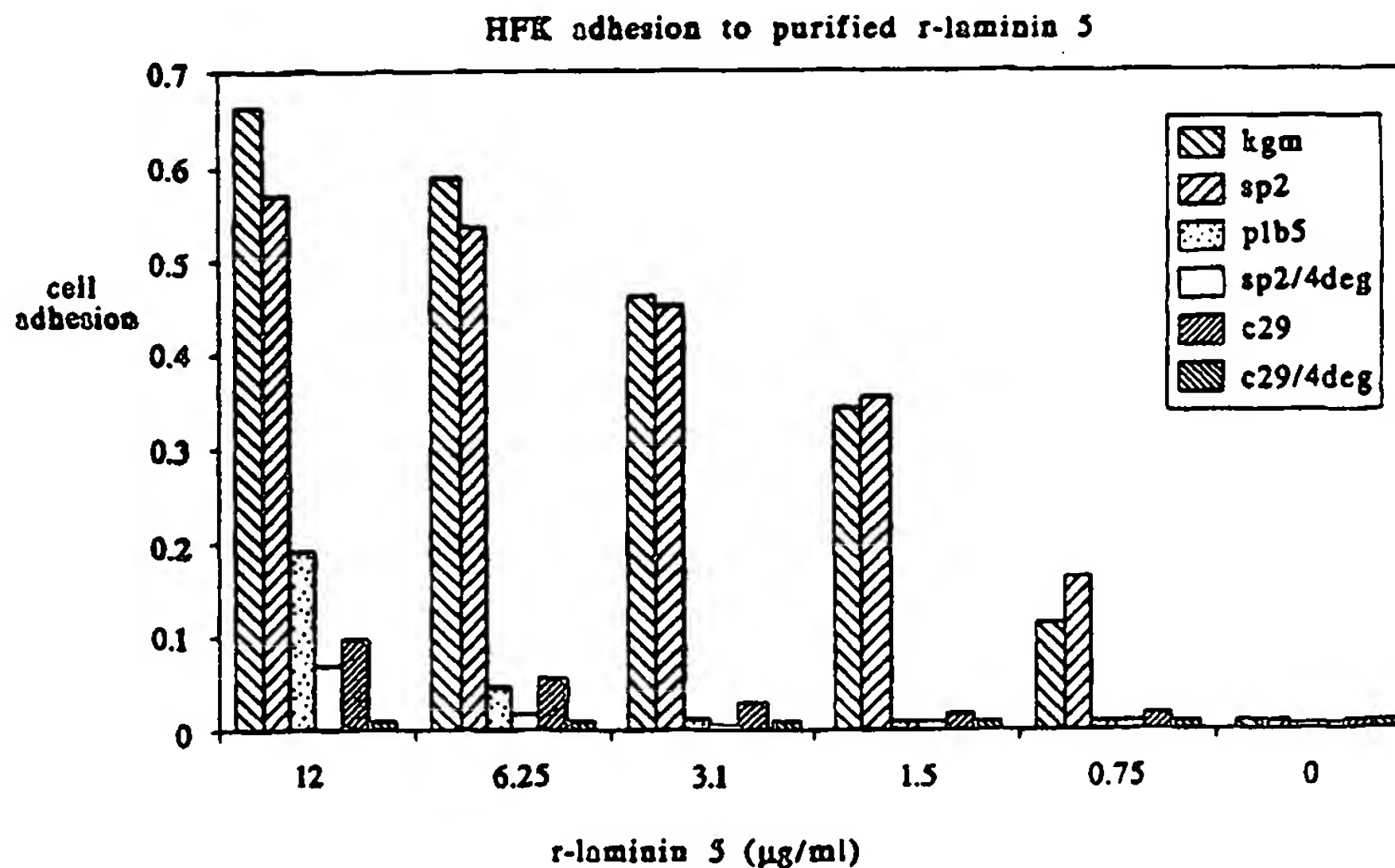




INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/12, 15/62, 5/10, C07K 14/78, A61K 38/39, A61P 3/10, 9/00, 17/02, A61L 29/00, 31/00		A2	(11) International Publication Number: WO 00/66731 (43) International Publication Date: 9 November 2000 (09.11.00)
(21) International Application Number: PCT/US00/11459 (22) International Filing Date: 28 April 2000 (28.04.00) (30) Priority Data: 60/131,720 30 April 1999 (30.04.99) US 60/149,738 21 August 1999 (21.08.99) US 60/155,945 24 September 1999 (24.09.99) US (71) Applicant (for all designated States except US): BIOSTATUM, INC. [US/US]; Suite 200, 4825 Creekstone Drive, Durham, NC 27703 (US). (72) Inventor; and (75) Inventor/Applicant (for US only): BOUTAUD, Ariel [CL/US]; Partners II Building, Suite 3700, 840 Main Campus Drive, Raleigh, NC 27606 (US). (74) Agent: HARPER, David, S.; McDonnell, Boehnen, Hulbert & Berghoff, Suite 3200, 300 South Wacker Drive, Chicago, IL 60606 (US).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published Without international search report and to be republished upon receipt of that report.	

(54) Title: RECOMBINANT LAMININ 5



(57) Abstract

The present invention provides recombinant laminin 5, methods for making recombinant laminin 5, cells that express recombinant laminin 5, and methods for using the recombinant laminin 5 to accelerate wound healing, and to promote cell attachment and migration.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

RECOMBINANT LAMININ 5

5 Cross Reference

This application claims priority to U.S. Provisional Patent Application Serial Nos. 60/131,720 filed April 30, 1999; 60/149,738 filed August 19, 1999; 60/155,945 filed September 24, 1999; and 60/182,012 filed February 11, 2000; all of which are incorporated herein by reference in their entirety.

10

Field of the Invention

This application relates to recombinant laminin 5 and methods for its use.

Background of the Invention

15

Basal laminae (basement membranes) are sheet-like, cell-associated extracellular matrices that play a central role in cell growth, tissue development, and tissue maintenance. They are present in virtually all tissues, and appear in the earliest stages of embryonic development.

20

Basal laminae are central to a variety of architectural and cell-interactive functions. (See for example, Malinda and Kleinman, *Int. J. Biochem. Cell Biol.* 28:957-959 (1996); Aumailley and Krieg, *J. Invest. Dermatology* 106:209-214 (1996)):

25

1. They serve as architectural supports for tissues, providing adhesive substrates for cells.

30

2. They create perm-selective barriers between tissue compartments that impede the migration of cells and passively regulate the exchange of macromolecules. These properties are illustrated by the kidney glomerular basement membrane, which functions as an important filtration structure, creating an effective blood-tissue barrier that is not permeable to most proteins and cells.

35

3. Basal laminae create highly interactive surfaces that can promote cell migration and cell elongation during embryogenesis and wound repair. Following an injury, they provide a surface upon which cells regenerate to restore normal tissue function.
4. Basal laminae present information encoded in their structure to contacting cells that is important for differentiation and tissue maintenance. This information is communicated to the cells through various receptors that include the integrins,

dystroglycan, and cell surface proteoglycans. Signaling is dependent not only on the presence of matrix ligands and corresponding receptors that interact with sufficient affinities, but also on such topographical factors as ligand density in a three-dimensional matrix "landscape", and on the ability of basal lamina components to cluster receptors. Because these matrix proteins can be long-lived, basal laminae
5 create a "surface memory" in the basal lamina for resident and transient cells.

The basal lamina is largely composed of laminin and type IV collagen heterotrimers that in turn become organized into complex polymeric structures. To date, six type IV
10 collagen chains and at least twelve laminin chains (and twelve different heterotrimeric laminins) have been identified. These chains possess shared and unique functions and are expressed with specific temporal (developmental) and spatial (tissue-site specific) patterns.

Laminins are a family of heterotrimeric glycoproteins that reside primarily in the basal lamina. They function via binding interactions with neighboring cell receptors, and
15 are important signaling molecules that can strongly influence cellular function. Laminins are important in both maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair and development.

Laminins are large, multi-domain proteins, with a common structural organization. The laminin molecule integrates various matrix and cell interactive functions into one
20 molecule.

The laminin molecule is comprised of α -, β -, and γ -chains joined together through a coiled-coil domain. Within this structure are identifiable domains that possess binding activity towards other laminin and basal lamina molecules, and membrane-bound receptors. Domains VI, IVb, and IVa form globular structures, and domains V, IIIb, and IIIa (which
25 contain cysteine-rich EGF-like elements) form rod-like structures. (Kamiguchi et al., Ann. Rev. Neurosci. 21:97-125 (1998)) Domains I and II of the three chains participate in the formation of a triple-stranded coiled-coil structure (the long arm).

Table 1 shows the individual chains that each laminin type is composed of:

30

TABLE 1. Known laminin family members

<i>Protein</i>	<i>Chains</i>
Laminin-1	$\alpha 1 \beta 1 \gamma 1$

Laminin-2	$\alpha 2\beta 1\gamma 1$
Laminin 3	$\alpha 1\beta 2\gamma 1$
Laminin-4	$\alpha 2\beta 2\gamma 1$
Laminin-5	$\alpha 3\beta 3\gamma 2$
Laminin-6	$\alpha 3\beta 1\gamma 1$
Laminin-7	$\alpha 3\beta 2\gamma 1$
Laminin-8	$\alpha 4\beta 1\gamma 1$
Laminin-9	$\alpha 4\beta 2\gamma 1$
Laminin-10	$\alpha 5\beta 1\gamma 1$
Laminin -11	$\alpha 5\beta 2\gamma 1$
Laminin-12	$\alpha 2\beta 1\gamma 3$

Four structurally-defined family groups of laminins have been identified. The first group of five identified laminin molecules all share the $\beta 1$ and $\gamma 1$ chains, and vary by their α -chain composition ($\alpha 1$ to $\alpha 5$ chain). The second group of five identified laminin molecules all share the $\beta 2$ and $\gamma 1$ chain, and again vary by their α -chain composition. The third group of identified laminin molecules has one identified member, laminin 5, with a chain composition of $\alpha 3\beta 3\gamma 2$. The fourth group of identified laminin molecules has one identified member, laminin 12, with the newly identified $\gamma 3$ chain ($\alpha 2\beta 1\gamma 3$)

Some progress has been made in elucidating the relationship between domain structure and function. (See, for example, Wewer and Engvall, *Neuromusc. Disord.* 6:409-418 (1996).) The overall sequence similarity among the homologous domains in different chains varies, but it is highest in domain VI (thought to play a key role in laminin polymerization), followed by domains V (possibly involved in protein-protein interactions) and III (entactin/nidogen binding; possible cell adhesion sites), and is lowest in domains I, II (both thought to be involved in intermolecular assembly, and containing possible cell adhesion sites), and G. Not all domains are present in all 3 types of chains. The globular G domain (thought to be involved in cell receptor binding) is present only in the α chains. Other domains may not be present in all chains within a certain chain type. For example, domain VI is absent from $\alpha 3$, $\alpha 4$, and $\gamma 2$ chains. (Wewer and Engvall, 1996)

As a result of their large size (>600 kD) and unique structure, the laminin molecules can be resolved in the electron microscope. (Wewer and Engvall, 1996) Typically, laminins appear as cross-shaped molecules in an EM. The three short arms of the cross represent the amino terminal portions of each of the three separate laminin chains (one short arm per chain). The long arm of the cross is composed of the C-terminal parts of the three chains, which together form a coiled coil structure. (Wewer and Engvall, 1996) The long arm ends with the globular G domain.

The coiled-coil domain of the long arm is crucial for assembly of the three chains of laminin. (Yurchenco et al., Proc. Natl. Acad. Sci. 94:10189-10194 (1997)). Disulfide bonds bridge and stabilize all three chains in the most proximal region of the long arm and join the β and γ chains in the most distal region of the long arm.

5 A model of laminin receptor-facilitated self-assembly, based on studies conducted with cultured skeletal myotubes and Schwann cells, predicts that laminins bind to their receptors, which freely diffuse in a fluidic membrane, when ligand-free. Receptor engagement forces these receptors into a high local two-dimensional concentration, facilitating their mass-action driven assembly into ordered surface polymers. In this process,
10 the engaged receptors are also reorganized, accompanied by cytoskeletal rearrangements. (Colognato, J. Cell Biol. 145:619-631 (1999)) This reorganization activates the receptors, causing signal transduction with the alteration of cell expression, shape and/or behavior.

One class of laminin receptors are the integrins, which are cell surface receptors that mediate many cell-matrix and cell-cell interactions. Integrins are heterodimers, consisting
15 of an α and a β subunit. 16 α - and 8 β -subunits are known, and at least 22 combinations of α and β subunits have been identified to date. Some integrins have only one or a few known ligands, whereas others appear to be very promiscuous. Binding to integrins is generally of low affinity, and is dependent on divalent cations. Integrins, activated through binding to their ligands, transduce signals via kinase activation cascades, such as focal
20 adhesion and mitogen-activated kinases. Several different integrins bind different laminin isoforms more or less specifically. (Aumailley et al., In The Laminins, Timpl and Ekblom, eds., Harwood Academic Publishers, Amsterdam. pp. 127-158 (1996))

Laminin-5, also referred to as kalinin, nicein, and epiligrin, plays a key role in modulating the behavior and activity of cells and tissues of epithelial origin, and is expected
25 to have broad uses in clinical settings where increased epithelial attachment and hemidesmosome assembly are required. (Takeda et al., J. Invest. Dermatol. 1999 113(1):38-42) Laminin-5 is a principal adhesive ligand in the epidermal basal lamina, and has been shown to promote the attachment of keratinocytes and epithelial cells to the basal lamina and underlying dermis, and also promotes hemidesmosome formation. (Burgeson et al. U.S.
30 Patent No. 5,770,562; Quaranta and Hormia, U.S. Patent No. 5,422,264; Jones, U.S. Patent No. 5,541,106; Quaranta and Hormia, U.S. Patent No. 5,658,789; Hormia et al., J. Invest. Dermatol. 1995 Oct. 105(4):557-561).

Laminin 5 is also thought to be necessary for the healing of epithelial tissue wounds. (Goldfinger et al., J. Cell Sci. 1999; 112(Pt. 16):2615-2629) Pretreatment of human keratinocyte sheets for grafting with laminin 5 improves grafting efficiency. (Takeda et al., J. Invest. Dermatol. 1999 Jul; 113(1):38-42). The addition of laminin-5 accelerates the formation of a basement membrane in a skin equivalent model (Tsunenaga et al., *Matrix Biol.* 17(8-9):603-613, 1998). Laminin-5 also promotes epithelial cell attachment to a wide variety of biomaterials, including polymers, hydroxyapatite, and metals. (Jones et al., U.S. Patent No. 5,585,267; El Ghannam et al., J. Biomed. Mater. Res. 1998 Jul; 41(1):30-40)

Laminin 5 has further been demonstrated to promote the following:

1. Epithelial cell adhesion to the internal basal lamina of teeth (Mullen et al., J. Periodontal. Res. 1999 Jan 34(1):16-24; Hormia et al., J. Dent. Res. 1998 Jul; 77(7):1479-1485) and anchorage of ameloblasts (ie: enamel-producing cells) to the enamel matrix. (Yoshida et al., Cell Tissue Res. 1998 Apr; 292(1):143-149)
2. Corneal epithelial cell adhesion. (Qin and Kurpakus, Exp. Eye Res. 1998 May 66(5):569-579)
3. Intestinal epithelial restitution. (Lotz et al., Am. J. Pathol. 1997 Feb; 150(2):747-760)
4. In vitro expansion of epithelial cells by providing an efficient adhesion substrate for primary cell cultures, thus providing the basis for a wide range of new cell therapy applications. (Gonzales et al., Mol. Biol. Cell. 1999 Feb; 10(2):259-270; Baker et al., Exp. Cell Res. 1996 Nov 1; 228(2):262-270).
5. Proliferation of pancreatic beta islet cells (Todorov et al., Transplant. Proc. 1998 Mar; 30(2): 455; Quaranta and Jones, U.S. Patent No. 5,510,263; Halberstadt et al., U.S. Patent No. 5,681,587; Halberstadt et al., U.S. Patent No. 5,672,361), and T cells (Vivinus-Nebot et al., J. Cell Biol. 1999 Feb 8; 144(3):563-574)

Thus, laminin 5 has broad uses in clinical settings where increased epithelial attachment and hemidesmosome assembly are required. Laminin 5 can be used to promote wound healing and tissue regeneration. The application of exogenous laminin 5 has broad application for the accelerated healing of skin disorders, such as diabetic foot ulcers, venous ulcers, pressure sores, skin surgery, burns, and acute wounds. Exogenous laminin 5 may be used to directly treat a wound surface, or may be applied to a variety of medical devices and dermal grafts for skin, corneal, gastrointestinal, and periodontal epithelial wound healing. The use of laminin 5 provides enhanced biocompatibility of the device or graft, which leads to improved tissue integration and remodeling, reduced immune response, and



reduced likelihood of infection. Laminin 5 is also useful for the ex vivo and in vitro proliferation of various cell types, including but not limited to epithelial cells, pancreatic beta islet cells, and T cells, and tissue equivalents. Thus, a source of laminin 5 for tissue culture media or a media supplement, as well as cell growth substrates coated with laminin 5, would
5 be particularly useful for the cultivation of these and other cell types.

A good source and purification procedure for laminin-5 is needed to provide material for the development of the therapeutic and research applications mentioned above. Some cell lines secrete laminin-5, and procedures have been developed to purify laminin-5 from the processed cells and cell media. However, these methods are time consuming and capable of
10 producing only small amounts of laminin 5. (Rouselle et al., J. Biol. Chem. 1995 270(23):13766-13770; Cheng et al., J. Biol. Chem. 1997, 272(50):31525-31532)

A preferred method of production, however, is the use of recombinant DNA technology to engineer a cell line of choice to produce recombinant laminin-5. A recombinant-based method of laminin-5 production has several advantages over purification
15 from tissue or isolation from cell lines in culture:

1. The recombinant produced protein is free of pathogens. While this is also true for endogenous cell culture produced protein, protein derived from human tissue carries a risk for contamination by HIV, hepatitis, and other infectious agents.
2. Expression levels of the protein, and hence yields, can be improved through
20 the use of genetically engineered genes/vectors that enhance the production of the encoded protein.
3. It is possible to engineer additional peptide sequences to the protein chain that provides a binding site for a commercially viable affinity purification procedure.
4. The method can provide for the modification of protein structure/function
25 through the addition, substitution, elimination, and/or other modifications of protein domain structures. For example, it may be desirable to introduce an integrin binding site (e.g. RGD), switch integrin recognition sites, or engineer in a stable binding site to a synthetic substrate. Thus, the creation of expression vectors that express laminin chains generates enormous flexibility for future uses and creates a basis for creating second
30 generation "designer" laminins.

Previous studies have produced cells transfected with one or two of the laminin 5 chain-encoding DNA sequences, but none have produced recombinant heterotrimeric laminin 5, not have they produced cell lines that secrete recombinant heterotrimeric laminin 5.

(Gagnoux-Palacios et al., J. Biol. Chem. 271:18437-18444 (1996); Matsui et al., J. Biol. Chem. 270:23496-23503 (1995))

Thus, there exists a need in the art for recombinant heterotrimeric laminin 5 protein, methods for making recombinant laminin 5, and methods of using recombinant laminin 5 for wound healing and tissue regeneration, for use on a variety of medical devices and dermal grafts for skin, corneal, gastrointestinal, and periodontal epithelial wound healing, for the ex vivo and in vitro proliferation of various cell types, and for tissue culture media, media supplements, and as a component of cell growth substrates.

Summary of the Invention

The present invention fulfills the need in the art for recombinant laminin 5 protein, methods for making recombinant laminin 5, and methods of using recombinant laminin 5 for the treatment of burns, for use on a variety of medical devices and dermal grafts for skin, corneal, gastrointestinal, and periodontal epithelial wound healing, for the ex vivo and in vitro proliferation of various cell types, and for tissue culture media, media supplements, and as a component of cell growth substrates.

In one aspect, the present invention provides cells that have been transfected with nucleic acid sequences encoding laminin $\alpha 3$, $\beta 3$ and $\gamma 2$ chains, wherein the cells express the individual chains, which assemble into heterotrimeric recombinant laminin-5 (hereinafter referred to as "r-laminin 5"). r-laminin 5, or processed forms thereof, are secreted by the cell.

In another aspect, the present invention provides r-laminin 5, and methods for producing substantially purified r-laminin 5, or processed forms thereof.

In a further aspect, the present invention provides pharmaceutical compositions, comprising r-laminin 5, or processed forms thereof, together with a pharmaceutically acceptable carrier. Such pharmaceutical compositions can optionally be provided with other compounds with wound healing and tissue regeneration utility, such as other extracellular matrix components.

In further aspect, the present invention provides methods and kits for using r-laminin 5 to:

- a. accelerate wound healing and tissue regeneration;
- b. enhance the performance of skin grafts;
- c. improve the attachment of gum tissue to the tooth surface;

- d. improve the biocompatibility of medical devices; and
- e. accelerate cell proliferation,

by providing an amount effective of r-laminin 5 for the various methods. The invention also provides methods and kits for using laminin 5 to regulate angiogenesis. The kits comprise an amount of laminin 5 or r-laminin 5 effective for the desired effect, and instructions for the use thereof.

In a further aspect, the present invention provides improved medical devices and grafts, wherein the improvement comprises coating the devices or grafts with an amount effective of r-laminin 5 or the pharmaceutical compositions of the invention for the desired application.

In a further aspect, the invention provides improved cell culture devices for the proliferation of cells in culture, by providing an amount effective of r-laminin 5 for the attachment of cells to a cell culture device for the attachment and subsequent proliferation, differentiation, or maintenance of the cells.

In another aspect, the invention provides a cell culture growth supplement, comprising r-laminin 5. In another aspect, the invention provides an improved cell culture growth media, wherein the improvement comprises the addition of r-laminin 5.

Brief Description of the Figures

Figure 1 is a bar graph showing the results of an HFK cell adhesion assay for r-laminin 5 activity in culture media from various clones.

Figure 2 is a bar graph showing a cell adhesion assay in which r-laminin 5 was coated directly onto the plate. p1b5 = anti-integrin $\alpha 3 \beta 1$ antibody; sp2 = control IgG, non-specific; C29: anti-laminin 5 antibody

Figure 3 is a rotary shadow analysis of r-laminin 5. Purified r-laminin 5 protein was diluted to 50 $\mu\text{g/ml}$ and adjusted to 70% glycerol/30% 0.15M ammonium bicarbonate and rotary shadowed using standard techniques. An approximately 80,000X magnification field is shown of (A) r-laminin 5; (B) "native" laminin 5 (purified by BM165 monoclonal antibody affinity chromatography from SCC-25 (squamous cell carcinoma cell line) conditioned medium). The bar represents 50 nm.

Detailed Description of the Preferred Embodiments

All references, patents and patent applications are hereby incorporated by reference in their entirety.

Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in *Methods in Enzymology* (M.P. Deutscher, ed., (1990) Academic Press, Inc.); *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, CA), *Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed.* (R.I. Freshney. 1987. Liss, Inc. New York, NY), *Gene Transfer and Expression Protocols*, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 1998 Catalog (Ambion, Austin, TX).

As used herein "laminin 5" encompasses both r-laminin 5 and heterotrimeric laminin 5 from naturally occurring sources.

The term "r-laminin 5" refers to include recombinant heterotrimeric laminin 5 expressed by a cell that has been exogenously transfected with expression vector(s) comprising polynucleotides that encode $\alpha 3$, $\beta 3$ and $\gamma 2$ laminin polypeptide chains, or a portion of each of the chains which are capable of forming a heterotrimeric laminin 5, as well as versions thereof resulting from cellular processing events. Such r-laminin 5 can comprise $\alpha 3$, $\beta 3$, and $\gamma 2$ sequences from a single organism, or from different organisms. Laminin 5 chain DNA sequences and their encoded proteins from a variety of organisms are known in the art. (See, for example, Gerecke et al., J. Biol. Chem. 269:11073-11080 (1994); Kallunki et al., J. Cell Biol. 119:679-693 (1992); Ryan et al., J. Biol. Chem. 269:22779-22787 (1994); Iivananinen et al., J. Biol. Chem. 274:14107-14111 (1999); Galliano et al., J. Biol. Chem. 270:21820-221826 (1995); Sugiyama et al., Eur. J. Biochem. 228:120-128 (1995) all references incorporated by reference herein in their entirety).

In the present invention, r-laminin 5 is a secreted protein, which is capable of being directed to the ER, secretory vesicles, and the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Such processing event can be variable, and thus may yield different versions of the final "mature

protein". The substantially purified r-laminin 5 of the present invention includes heterotrimers comprising both the full length and any such processed laminin 5 chains.

As used herein, the term "substantially purified" means that the recombinant laminin 5 so designated has been separated from its in vivo cellular environments.

5 As used herein, a laminin 5 polypeptide chain refers to a polypeptide chain according to one or more of the following:

(a) comprises a polypeptide structure selected from the group consisting of:

1. R1-R2-R3
2. R1-R2-R3(e)
- 10 3. R3
4. R3(e)
5. R1-R3
6. R1-R3(e)
7. R2-R3
- 15 8. R2-R3(e)

wherein R1 is a amino terminal methionine; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, an artificial sequence; R3 is a secreted laminin chain selected from the $\alpha 3$, $\beta 3$, and $\gamma 2$ chains; 20 and R3(e) is a secreted laminin chain selected from the $\alpha 3$, $\beta 3$, and $\gamma 2$ chains that further comprises an epitope tag (such as those described below), which can be placed at any position within the laminin chain amino acid sequence; and/or

(b) is encoded by a polynucleotide that is substantially similar to the disclosed laminin polynucleotide sequences or portions thereof (SEQ ID NOS.: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 25 21, 23, 25, 27, 29, 31, 33, 35); and/or

(c) is encoded by a polynucleotide that hybridizes under high or low stringency conditions to coding regions, or portions thereof, of one or more of the recombinant laminin 5 chain DNA sequences disclosed herein (SEQ ID NOS.: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35), or complementary sequences thereof; and/or

30 (d) has at least 70% identity to the disclosed laminin polypeptide claim amino acid sequences (SEQ ID NOS.: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36), preferably at least 80% identity, and most preferably at least about 90% identity.

The phrase "substantially similar" is used herein in reference to polynucleotide or polypeptide sequences having one or more conservative variations from the laminin 5 sequences disclosed herein, including but not limited to deletions, insertions, inversions, repeats, and substitutions, wherein the resulting laminin chain is functionally equivalent to those disclosed herein.

For example, conservative polynucleotide variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, including but not limited to optimizing codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring conservative variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level. Alternatively, non-naturally occurring conservative variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, conservative polynucleotide variants may be generated to improve or alter the characteristics of the expressed laminin chain polypeptides. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein. (See, for example, Ron et al., J. Biol. Chem. 268: 2984-2988 (1993); Dobeli et al., J. Biotechnology 7:199-216 (1988)) Ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. (See, for example, Gayle et al., J. Biol. Chem 268:22105-22111 (1993)) Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained.

Guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different

species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still
5 maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells,
10 Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most
15 buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn
20 and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

The "substantially similar" polypeptides of the present invention also include (i) substitutions with one or more of the non-conserved amino acid residues, where the
25 substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group; (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol); and/or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region
30 peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved
35 characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity.

(Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

"Stringency of hybridization" is used herein to refer to conditions under which nucleic acid hybrids are stable. The invention also includes nucleic acids that hybridize under high stringency conditions (as defined herein) to all or a portion of the coding sequences of the laminin chain polynucleotides disclosed herein, or their complements. The hybridizing portion of the hybridizing nucleic acids is typically at least 50 nucleotides in length. As known to those of skill in the art, the stability of hybrids is reflected in the melting temperature (T_M) of the hybrids. T_M decreases approximately 1-1.5°C with every 1% decrease in sequence homology. In general, the stability of a hybrid is a function of sodium ion concentration and temperature. Typically, the hybridization reaction is performed under conditions of lower stringency, followed by washes of varying, but higher, stringency. Reference to hybridization stringency relates to such washing conditions. Thus, as used herein, high stringency refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are laminin 5-encoding nucleic acid sequences that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

As used herein, "percent identity" of two amino acids or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3, to obtain an amino acid sequence homologous to a polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids. Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. See <http://www.ncbi.nlm.nih.gov>.

Further embodiments of the present invention include polynucleotides encoding laminin chain polypeptides having at least 70% identity, preferably at least 80% identity, and most preferably at least 90% identity to one or more polypeptide sequences, or fragments thereof, contained in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34.

As used herein, " α 3 polynucleotide" refers to polynucleotides encoding an α 3 laminin chain of the same name. Such polynucleotides can be characterized by one or more of the following: (a) the nucleotides of said polynucleotide may encode an amino acid sequence substantially similar to one or more of the sequences set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12 or fragments thereof, or fragments thereof; (b) polynucleotides that encode polypeptides which share at least 70% identity, preferably 80% identity, and most preferably at least 90% identity with one or more of the sequences set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12 or fragments thereof; (c) the α 3 polynucleotides hybridize under low or high stringency conditions to the coding sequence set forth in one or more of SEQ ID NO: 1, 3, 5, 7, 9, 11, fragments thereof, or complementary sequences thereof; (d) the α 3 polynucleotides may encode a polypeptide with a general structure selected from (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e); wherein R1 and R2 are as described above, and R3 and R3(e) are as described above but comprise secreted α 3 chain polypeptides.

As used herein, " β 3 polynucleotide" refers to polynucleotides encoding a β 3 laminin chain of the same name. Such polynucleotides can be characterized by one or more of the following: (a) the nucleotides of said polynucleotide may encode an amino acid sequence substantially similar to one or more of the sequences set forth in SEQ ID NO: 14, 16, 18, 20, 22, 24, or fragments thereof; (b) polynucleotides that encode polypeptides which share at least 70% identity, preferably at least 80%, and most preferably at least 90% identity with one or more of the sequences set forth in SEQ ID NO: 14, 16, 18, 20, 22, 24, or fragments thereof; (c) the β 3 polynucleotides hybridize under low or high stringency conditions to the coding sequence of one or more of the sequences set forth in SEQ ID NO: 13, 15, 17, 19, 21, 23, fragments thereof or complementary sequences thereof; (d) the β 3 polynucleotides may encode a polypeptide with a general structure selected from (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e); wherein R1 and R2 are as described above, and R3 and R3(e) are as described above but comprise secreted β 3 chain polypeptides.

As used herein, " γ 2 polynucleotide" refers to polynucleotides encoding a γ 2 laminin chain of the same name. Such polynucleotides can be characterized by one or more of the following: (a) the nucleotides of said polynucleotide may encode an amino acid that is substantially similar to one or more of the sequences set forth in SEQ ID NO: 26, 28, 30, 32, 34, 36 or fragments thereof; (b) polynucleotides that encode polypeptides which share at least 70% identity, preferably at least 80%, and most preferably at least 90% identity with one or more of the sequences set forth in SEQ ID NO: 26, 28, 30, 32, 34, 36 or fragments thereof; (c) the γ 2 polynucleotides hybridize under low or high stringency conditions to the coding sequence set forth in one or more of SEQ ID NO: 25, 27, 29, 31, 33, 35, fragments thereof, or complementary sequences thereof; (d) the γ 2 polynucleotides may encode a polypeptide with a general structure selected from (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e); wherein R1 and R2 are as described above, and R3 and R3(e) are as described above but comprise secreted γ 2 chain polypeptides.

As used herein, the term "epitope tag" refers to a polypeptide sequence that is expressed as part of a chimeric protein, where the epitope tag serves as a recognition site for binding of antibodies generated against the epitope tag, or for binding of other molecules that can be used for affinity purification of sequences containing the tag.

As used herein, the term "increased biocompatibility" refers to reduced induction of acute or chronic inflammatory response, and reduced disruption of the proper differentiation

of implant-surrounding tissues for laminin 5-coated biomaterials relative to an analogous, non-coated biomaterial.

As used herein the term "graft" refers to both natural and prosthetic grafts and implants.

5 In one aspect, the present invention provides cells that have been systematically transfected with recombinant expression vectors comprising promoter sequences that are operatively linked to polynucleotide sequences encoding polypeptide sequences comprising $\alpha 3$, $\beta 3$, and $\gamma 2$ laminin 5 chains. After the multiple transfections, the cells express each of the recombinant laminin 5 chains, which assemble into a heterotrimer and can be purified from
10 the cell culture medium.

In a preferred embodiment, cDNAs encoding proteins comprising the $\alpha 3$, $\beta 3$, and $\gamma 2$ laminin polypeptide chains, or fragments thereof, are subcloned into an expression vector. Alternatively, laminin 5 $\alpha 3$, $\beta 3$, and/or $\gamma 2$ gene sequences, including one or more introns, and including various 5' and 3' non-coding regions, can be used.

15 Any cell capable of expressing and secreting the r-laminin 5 can be used. Preferably, eukaryotic cells are used, and most preferably mammalian cells are used, including but not limited to kidney and epithelial cell lines. Especially preferred are those mammalian cells that do not endogenously express laminin 5. Carbohydrate and disulfide post-translational modifications are believed to be required for laminin 5 protein folding and function. This
20 makes the use of eukaryotic cells preferable for producing functional r-laminin 5, although other systems are useful for obtaining, for example, antigens for antibody production.

"Recombinant expression vector" includes vectors that operatively link a nucleic acid coding region or gene to any promoter capable of effecting expression of the gene product. The promoter sequence used to drive expression of the laminin 5 individual chains may be
25 constitutive (driven by any of a variety of promoters, including but not limited to, CMV, SV40, RSV, actin, EF) or inducible (driven by any of a number of inducible promoters including, but not limited to, tetracycline, ecdysone, steroid-responsive). The expression vector must be replicable in the host organisms either as an episome or by integration into host chromosomal DNA. In a preferred embodiment, the expression vector comprises a
30 plasmid. However, the invention is intended to include other expression vectors that serve equivalent functions, such as viral vectors.

In one embodiment, at least one of the laminin chain polypeptide sequences, or fragments thereof, is operatively linked to a nucleic acid sequence encoding an "epitope tag",

so that at least one of the chains is expressed as a fusion protein with an expressed epitope tag. The epitope tag may be expressed as the amino terminus, the carboxy terminus, or internal to the end of a r-laminin 5 chain, so long as the resulting heterotrimeric r-laminin 5 remains functional. Any epitope tag may be utilized, so long as it can be used as the basis for
5 affinity purification of the resulting r-laminin 5 heterotrimer. Examples of such epitope tags include, but are not limited to FLAG (Sigma Chemical, St. Louis, MO), myc (9E10) (Invitrogen, Carlsbad, CA), 6-His (Invitrogen; Novagen, Madison, WI), and HA (Boehringer Mannheim Biochemicals).

In another embodiment, one of the r-laminin 5 chains is expressed as a fusion protein
10 with a first epitope tag, and at least one other r-laminin chain is expressed as a fusion protein with a second epitope tag. This permits multiple rounds of purification to be carried out. Alternatively, the same epitope tag can be used to create fusion proteins with more than one of the r-laminin chains.

In a further embodiment, the epitope tag can be engineered to be cleavable from the
15 r-laminin 5 chain(s). Alternatively, no epitope tag is fused to any of the r-laminin 5 chains, and the r-laminin 5 is purified by standard chromatography techniques, including but not limited to affinity chromatography using laminin 5 specific antibodies or other laminin 5 binding molecules, ionic exchange, hydrophobic exchange, etc.

Transfection of expression vectors into the host cells can be accomplished via any
20 technique known in the art, including but not limited to standard bacterial transformation, calcium phosphate co-precipitation, electroporation, or liposome mediated-, DEAE dextran mediated-, polycationic mediated-, or viral mediated transfection.

In a preferred embodiment, the cells are stably transfected. Any methods for stable
25 transfection and selection of appropriate transfected cells are known in the art. In a most preferred embodiment, a CMV promoter driven expression vector is used in a human kidney embryonic 293 cell line.

Media from cells transfected with a single laminin chain are initially analyzed on
Western blots using chain-specific anti-laminin-5 antibodies. The expression of single
laminin chains following transfection is generally intracellular. Clones showing reactivity
30 against individual transfected chain(s) are verified by any appropriate method, such as PCR, reverse transcription-PCR, or nucleic acid hybridization, to confirm incorporation of the transfected gene. Preferably, analysis of genomic DNA preparations from such clones is done by PCR using laminin chain-specific primer pairs. Media from transfected clones producing all three chains are further analyzed for heterotrimeric laminin 5 secretion and/or

activity, by any appropriate method, including Western blot analysis and cell binding assays, such as a keratinocyte cell adhesion assay.

In another aspect, the present invention provides substantially purified r-laminin 5, comprising an $\alpha 3$ chain, a $\beta 3$ chain, and a $\gamma 2$ chain, and methods for producing substantially purified r-laminin 5. In one embodiment, the r-laminin 5 comprises a first chain comprising a polypeptide that is substantially similar to at least one of the sequences shown in SEQ ID NO:2, 4, 6, 8, 10, 12 or fragments thereof; a second chain comprising a polypeptide that is substantially similar to at least one of the sequences shown in SEQ ID NO:14, 16, 18, 20, 22, 24, or fragments thereof; and a third chain comprising a polypeptide that is substantially similar to at least one of the sequences shown in SEQ ID NO:26, 28, 30, 32, 34, 36, or fragments thereof, wherein the first, second, and third polypeptides are produced recombinantly, and wherein the first, second, and third chains assemble into a recombinant heterotrimeric laminin 5.

In another embodiment, the substantially purified r-laminin 5 comprises a first chain comprising a polypeptide that is at least about 70% identical to at least one of the sequences shown in SEQ ID NO:2, 4, 6, 8, 10, 12, or fragments thereof; a second chain comprising a polypeptide that is at least 70% identical to at least one of the sequences shown in SEQ ID NO:14, 16, 18, 20, 22, 24, or fragments thereof; and a third chain comprising a polypeptide that is at least 70% identical to at least one of the sequences shown in SEQ ID NO:26, 28, 30, 32, 34, 36, or fragments thereof, wherein the first, second, and third polypeptides assemble into a recombinant heterotrimeric laminin 5.

In a preferred embodiment, at least one of the first, second, or third chains of the substantially purified human r-laminin 5 is expressed as a fusion protein with an epitope tag.

Alternatively, the r-laminin 5 comprises a heterotrimeric polypeptide structure, wherein each individual chain comprises a general structure selected from the group consisting of: (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e)

wherein R1 is a amino terminal methionine; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, or an artificial sequence; R3 is a secreted $\alpha 3$, $\beta 3$, or $\gamma 2$ laminin chain; and R3(e) is a secreted laminin $\alpha 3$, $\beta 3$, and $\gamma 2$ chain that further comprises an epitope tag (such as those described above), which can be placed at any position within the laminin chain amino acid sequence.

In a preferred embodiment, purification of the r-laminin 5 is accomplished by passing media from the transfected cells through an affinity column. For example, antibodies or other binding molecules that bind to a peptide epitope expressed on at least one of the recombinant chains are attached to an affinity column, and bind r-laminin 5 that has been secreted into the media. The r-laminin 5 is removed from the column by passing excess peptide through the column. The eluted protein can subsequently be further purified, if desired.

Eluted fractions are analyzed by any appropriate method, including gel electrophoresis and Western blot analysis. In a further embodiment, the peptide epitope can be cleaved after purification. In other embodiments, two or three separate r-laminin chains are expressed as fusion proteins, each with a different epitope tag, permitting two or three rounds of purification and a doubly or triply purified r-laminin 5. The epitope tag can be engineered so as to be cleavable from the r-laminin 5 chain(s) after purification. Alternatively, no epitope tag is fused to any of the r-laminin 5 chains, and the r-laminin 5 is purified by standard techniques, including but not limited to affinity chromatography using laminin 5 specific antibodies or other laminin 5 binding molecules.

In another aspect, the present invention provides novel laminin $\beta 3$ and $\gamma 2$ chain nucleic acids and proteins, consisting of the nucleic acid sequences and proteins disclosed as SEQ ID NO:21-22, 23-24, 29-30, and 31-32.

The present invention further provides pharmaceutical compositions comprising r-laminin 5, as disclosed above, and a pharmaceutically acceptable carrier. According to this aspect of the invention, other agents can be included in the pharmaceutical compositions, depending on the condition being treated, including but not limited to any of the collagens, other laminin types, fibronectin, integrins, glycoproteins, proteoglycans, heparan and heparan sulfate proteoglycans, growth factors such as vascular endothelial growth factor (VEGF), platelet derived growth factor (PDGF), and keratinocyte growth factor (KGF); glycosaminoglycans, entactin, nidogen, and peptide fragments thereof.

Pharmaceutical preparations comprising r-laminin 5 can be prepared in any suitable form, and generally comprise the r-laminin 5 in combination with any of the well known pharmaceutically acceptable carriers. The carriers can be injectable carriers, topical carriers, transdermal carriers, and the like. The preparation may advantageously be in a form for topical administration, such as an ointment, gel, cream, spray, dispersion, suspension or paste. The preparations may further advantageously include preservatives, antibacterials, antifungals, antioxidants, osmotic agents, and similar materials in composition and quantity

as is conventional. Suitable solutions for use in accordance with the invention are sterile, are not harmful for the proposed application, and may be subjected to conventional pharmaceutical operations such as sterilization and/or may contain conventional adjuvants, such as preservatives, stabilizers, wetting agents, emulsifiers, buffers etc. For assistance in
5 formulating the compositions of the present invention, one may refer to Remington's Pharmaceutical Sciences, 15th Ed., Mack Publishing Co., Easton, Pa. (1975).

The dosage regimen for various treatments using the r-laminin 5 of the present invention is based on a variety of factors, including the type of injury or condition, the age, weight, sex, medical condition of the individual, the severity of the condition, and the route
10 of administration. Thus, the dosage regimen may vary widely, but can be determined routinely by a physician using standard methods. Laminins are extremely potent molecules, and one or a few molecules per cell could produce an effect. Thus, effective doses in the pico-gram per milliliter range are possible if the delivery is optimized. Laminins are sometimes present in an insoluble form in the basement membrane and have the capability of
15 polymerizing at concentrations ranging as low as about 50 $\mu\text{g/ml}$, depending on the laminin isoform and the conditions. Laminins can also polymerize into a gel at a concentration of 2-3 mg/ml. Dosage levels of the order of between 1 ng/ml and 10 mg/ml are thus useful for all methods disclosed herein, preferably between about 1 $\mu\text{g/ml}$ and about 3 mg/ml.

The treatment regime will also vary depending on the condition of the subject, based
20 on a variety of factors, including the type of injury, the age, weight, sex, medical condition of the individual, the severity of the condition, and the route of administration. For example, r-laminin 5 can be used to coat a wound dressing, which is placed in contact with a patient's wound as frequently as the dressing needs to be changed, and for as long as the dressing is applied to the wound surface.

25 Similarly, the route of administration will vary depending on the condition of the subject, based on a variety of factors, including the type of injury, the age, weight, sex, medical condition of the individual, and the severity of the condition.

In further aspect, the present invention provides methods for using r-laminin 5, or the pharmaceutical compositions of the invention, to accelerate wound healing and tissue
30 regeneration. In preferred embodiments, r-laminin 5 is used to accelerate the healing of skin in diabetic foot ulcers, venous ulcers, pressure sores, skin surgery, severe burns, and acute wounds, and enhanced performance of skin grafts (both autologous and artificial). In another aspect, the present invention provides kits for carrying out these methods, comprising an

amount effective of laminin 5 or r-laminin 5 and instructions for using the laminin 5 to carry out the methods.

In one embodiment, r-laminin 5, or a pharmaceutical composition comprising r-laminin 5, is used to enhance wound healing by promoting the adhesion of transplanted
5 cultured keratinocytes or other epithelial cells to an underlying substrate, such as a mammalian or human dermis. The substrate may comprise a wound surface, the basal surface of a confluent layer of cultured epithelial cells to be transplanted, or a substrate to be applied to the wound surface, such as a wound dressing, prior to placing the layer on a graft site. The r-laminin 5 may be supplied in a pharmaceutically acceptable carrier, preferably in amounts
10 of between about 1 ng/ml and about 10 mg/ml.

The use of kalinin-containing (ie: laminin 5-containing) isolated cell matrices has previously been shown to enhance the adhesion of transplanted cultured keratinocytes to an underlying substrate (Burgeson et al., US Patent No. 5,770,562). This and other studies have thus demonstrated that laminin 5 stimulates epithelial cell attachment and spreading, and thus
15 provides an appropriate surface facilitating the healing of skin and the use of skin grafts. (Quaranta and Hormia, U.S. Patent No. 5,422,264; Jones, U.S. Patent No. 5,541,106; Quaranta and Hormia, U.S. Patent No. 5,658,789; Hormia et al., J. Invest. Dermatol. 1995 Oct. 105(4):557-561; Takeda et al., J. Invest. Dermatol. 1999 Jul; 113(1):38-42; Goldfinger et al., J. Cell Sci. 1999; 112(Pt. 16):2615-2629).

Thus, the addition of r-laminin 5 to the appropriate injured tissue can promote cell
20 growth, cell migration, and accelerate tissue regeneration. Accelerated healing has the added benefit of reducing inflammatory responses and scarring. This can be accomplished in some cases by simply coating the r-laminin 5 or the pharmaceutical compositions of the invention into a wound area (such as skin, periodontal epithelial cells), or in other cases, by
25 providing a suitable substrate to which r-laminin 5 has been anchored, including but not limited to wound dressing and matrices, graft substrates, and dental abutments.

The incorporation of recombinant r-laminin 5 into wound repair dressings and matrices as well as tissue grafts will provide a natural ligand interactive surface to promote normal cell adherence, cell growth and tissue development. Many grafts are used to replace
30 tissue that has an epithelial cell layer adherent to a basal lamina. When an inappropriate surface is provided to these cells following grafting, the graft is at risk for failure of restoration of the normal cell layer. The advantage of coating these grafts with r-laminin 5 is to create a surface that sufficiently recapitulates a normal basal lamina surface to promote cell re-population.

Skin grafts are used in cases where large surface areas of skin have been burned or injured. The application of r-laminin 5 and/or the pharmaceutical compositions of the invention will significantly promote the attachment and 'take' of skin grafts to the injured tissue, as well as promote normal skin healing processes while minimizing scar tissue formation.

Collagen-based matrices are also applied to serious skin injuries to promote the growth of the underlying dermis and improve the take of a skin graft. Coating the collagen matrices with r-laminin-5 will create a more natural ligand interactive surface to promote cell migration, cell proliferation and the regeneration of the dermis. An acceleration of the regeneration of the dermis, and take of the skin graft, will minimize scar tissue formation.

Purified laminin 5 has been demonstrated to support epithelial cell adhesion to the internal basal lamina of teeth (Mullen et al., J. Periodontal. Res. 1999 Jan 34(1):16-24; Hormia et al., J. Dent. Res. 1998 Jul; 77(7):1479-1485) and is believed to strengthen the anchorage of ameloblasts (ie: enamel-producing cells) to the enamel matrix. (Yoshida et al., Cell Tissue Res. 1998 Apr; 292(1):143-149). Thus, in another embodiment, the r-laminin 5 or the pharmaceutical compositions of the invention are used to stimulate epithelium cell adhesion to the internal basal lamina of teeth and of ameloblasts to the enamel matrix of teeth. Such treatments are useful for the treatment of periodontal diseases, including but not limited to oral ulcerations, gingivitis and periodontitis. For example, existing teeth may be coated with the r-laminin 5 or the pharmaceutical compositions of the present invention as a treatment for gum (junctional epithelium) diseases, including but not limited to gingivitis and periodontitis, which promote the detachment of the gum from the tooth. These disease conditions allow the accumulation of food and other foreign matter in the space between the gum and the tooth, resulting in infection. The r-laminin 5 will promote reattachment of the gum to the tooth, thus preventing entry of foreign matter and subsequent infection.

For use in treating gingivitis and other periodontal diseases and disorders, the pharmaceutical compositions of the present invention may be in the form of toothcreams, toothpastes, liquid dentifrices, tooth-powders chewing-gum, tablets and the like. The pharmaceutical compositions of the invention can also contain flavoring, coloring agents, sweeteners, preservatives, surface active agents, and the like.

Purified laminin-5 has been shown to promote the *in vitro* expansion of epithelial cells (Gonzales et al., Mol. Biol. Cell. 1999 Feb; 10(2):259-270; Baker et al., Exp. Cell Res. 1996 Nov 1; 228(2):262-270), pancreatic beta islet cells (Todorov et al., Transplant. Proc. 1998 Mar; 30(2): 455; Quaranta and Jones, U.S. Patent No. 5,510,263; Halberstadt et al, U.S.

Patent No. 5,681,587; Halberstadt et al., U.S. Patent No. 5,672,361), and T cells (Vivinus-Nebot et al., J. Cell Biol. 1999 Feb 8; 144(3):563-574), by providing an efficient adhesion substrate for primary cell cultures. Thus, in another aspect of the present invention, r-laminin 5 is used to enhance the adhesion of cells for proliferation, differentiation, or maintenance of cells including, but not limited to pancreatic beta islet cells, epithelial cells, or T cells, by contacting the cells with an amount effective of r-laminin 5 to provide an efficient adhesion substrate for attachment and subsequent proliferation, differentiation, or maintenance of the cells. The r-laminin 5 can be provided in the cell culture medium, as a cell culture medium supplement, or may be coated on the surface of a cell growth substrate. In each case, r-laminin 5 is preferably used at a concentration of between about 1 ng/ml and about 10 mg/ml. The cells can optionally be contacted with other compounds that promote cell adhesion, proliferation, differentiation, and/or maintenance, including but not limited to any of the collagens, other laminin types, fibronectin, integrins, glycoproteins, proteoglycans, heparan sulfate proteoglycan, glycosaminoglycans, entactin, nidogen, and peptide fragments thereof.

The cells may be primary cells or cell lines. The methods of this aspect of the invention can be used in vivo, ex vivo, or in vitro.

In a preferred embodiment, r-laminin 5 is used to coat the surface of a substrate to promote cell adhesion to the substrate, and to stimulate cell proliferation, differentiation, and/or maintenance. The substrate used herein may be any desired substrate. For laboratory use, the substrate may be as simple as glass or plastic. For use in vivo, the substrate may be any biologically compatible material capable of supporting cell growth. Suitable substrate materials include shaped articles made of or coated with such materials as collagen, regenerated collagen, polyglycolic acid, polygalactose, polylactic acid or derivatives thereof; biocompatible metals such as titanium and stainless steel; ceramic materials including prosthetic material such as hydroxylapatite; synthetic polymers including polyesters and nylons; polystyrene; polyacrylates; polytetrafluoroethylene, and virtually any other material to which biological molecules can readily adhere. The determination of the ability of a particular material to support adhesion of r-laminin 5 of the invention requires only routine experimentation by the skilled artisan.

In a further aspect, the present invention provides a method of treating Type I diabetes in a patient in need thereof comprising contacting pancreatic beta islet cells with an amount effective of r-laminin 5 to provide an efficient adhesion substrate for the cells, leading to increased proliferation of insulin-producing pancreatic beta islet cells, and administering the cells to a patient in need thereof.

Nearly two million Americans are afflicted with Type I (insulin-dependent) diabetes, in which the pancreas has lost its ability to secrete insulin due to an autoimmune disorder in which the insulin-secreting beta cells, found within the islet cells of the pancreas, are destroyed. Although insulin injections can compensate for beta cell destruction, blood sugar
5 levels can still fluctuate dramatically. The impaired ability to take up glucose from the blood results in side reactions in which toxic products accumulate, leading to complications including blindness, kidney disease, nerve damage, and, ultimately, coma and death.

(U.S. Patent No. 5,672,361)

The pancreatic beta islet cells to be grown are plated on or applied to the matrix-
10 coated substrate using standard tissue culture techniques, followed by expansion in standard cell growth medium (as disclosed in U.S. Patent No. 5,672,361) in the presence of r-laminin 5. Any medium capable of supporting the enhanced growth of adult islet cells on the matrix-coated substrate is within the scope of the invention, as discussed above.

Fetal pancreatic islet cells may be grown in vitro in the presence of r-laminin 5 for
15 transplantation into diabetic patients. Growth of fetal pancreatic islet cells in the presence of r-laminin 5 increases the yield of islet cells for transplantation and thus solves the need to produce larger amounts of these cells. In addition, it is contemplated that the inclusion of other growth factors in the adult islet cell culture medium will further increase the yield of islet cells.

20 Laminins, or cell extracts containing laminins have been shown to regulate angiogenesis in a biphasic manner. (See, for example, Nicosia et al., Dev. Biol. 164:197-206 (1994); Bonfil et al., Int. J. Cancer 58:233-239 (1994)). At lower concentrations (30-300 $\mu\text{g/ml}$), a laminin-entactin complex stimulated angiogenesis in a three-dimensional culture, while at 3000 $\mu\text{g/ml}$ the same complex was inhibitory to angiogenesis. Thus, in another
25 aspect, the present invention provides methods for regulating angiogenesis, comprising contacting a tissue or culture substrate with an amount effective of laminin 5 or pharmaceutical compositions thereof to regulate angiogenesis. In one embodiment, the laminin 5 is used to promote angiogenesis by contacting a tissue or culture substrate with an amount effective of laminin 5 to promote angiogenesis. In another embodiment, the laminin
30 5 is used to inhibit angiogenesis, by contacting the tissue or culture substrate with an amount effective of laminin 5 to inhibit angiogenesis. An example of culture substrates to be contacted with laminin 5 to regulate angiogenesis are those used for tissue engineering purposes.

As used herein, the term "angiogenesis" refers to the formation of blood vessels. Specifically, angiogenesis is a multistep process in which endothelial cells focally degrade and invade through their own basement membrane, migrate through interstitial stroma toward an angiogenic stimulus, proliferate proximal to the migrating tip, organize into blood vessels, and reattach to newly synthesized basement membrane (see Folkman et al., Adv. Cancer Res., Vol. 43, pp. 175-203 (1985)). Compounds that promote angiogenesis can be used to promote wound healing and skin grafting, organ transplantation (including artificial organs), acceleration of endothelial cell coverage of vascular grafts to prevent graft failure due to re-occlusion, to treat ischemic conditions, and to treat inflammatory diseases.

10 In a further aspect, the present invention provides cell substrates comprising an amount effective of r-laminin 5 for the adhesion, growth, or maintenance of cells in culture,. The substrates may comprise any of the substrates discussed above. Preferably, the r-laminin 5 is coated on the surface of the substrate using solution at a concentration of between about 1 ng/ml and about 10 mg/ml.

15 In another aspect of the present invention, an improved cell culture medium is provided, wherein the improvement comprises addition to the cell culture medium of an effective amount of r-laminin 5 to the cell culture medium to promote the adherence, proliferation, and/or maintenance of cells. Any cell culture media that can support the growth of cells can be used with the present invention. Such cell culture media include, but are not limited to Basal Media Eagle, Dulbecco's Modified Eagle Medium, Iscove's Modified
20 Dulbecco's Medium, McCoy's Medium, Minimum Essential Medium, F-10 Nutrient Mixtures, Opti-MEM® Reduced-Serum Medium, RPMI Medium, and Macrophage-SFM Medium or combinations thereof.

The improved cell culture medium can be supplied in either a concentrated (ie: 10X) or non-concentrated form, and may be supplied as either a liquid, a powder, or a lyophilizate. The cell culture may be either chemically defined, or may contain a serum supplement. Culture media is commercially available from many sources, such as GIBCO BRL (Gaithersburg, MD) and Sigma (St. Louis, MO). Alternatively, the r-laminin 5 is used as a cell culture supplement, and can be separately added to the cell culture medium.

30 Purified laminin-5 has also been shown to promote epithelial cell attachment to a wide variety of biomaterials, including polymers, hydroxyapatite, and metals, thus improving the biocompatibility of the biomaterials. (Jones et al., U.S. Patent No. 5,585,267; El Ghannam et al., J. Biomed. Mater. Res. 1998 Jul; 41(1):30-40)

Thus, in a further aspect, the present invention comprises medical devices with improved biocompatibility, wherein the devices are coated with the r-laminin 5 of the invention, alone or in combination with other proteins or agents that serve to increase the biocompatibility of the device surface. The coated device stimulates cell attachment and provides for diminished inflammation and/or infection at the site of entry of the appliance. The device may also be used to stimulate gum junctional epithelium adhesion in the treatment of gingivitis and periodontitis.

Preferably, the device is a shaped article that is either an indwelling or transcutaneous catheter, polytetrafluoroethylene (PTFE), expanded PTFE (EPTFE), needle, metal pin, metal rod, colostomy tube, transcutaneous catheter, dental abutment piece or surgical mesh. In another aspect of this preferred embodiment, the device is used in vivo. Preferably, the appliance is made of or coated with a biocompatible metal that may be either stainless steel or titanium. Alternatively, the device is made of or coated with a ceramic material, or a polymer including but not limited to polyester, polyglycolic acid or a polygalactose-polyglycolic acid copolymer.

One particular use of the present invention is to increase epithelial cell adhesion to target surfaces. For example, prostheses for dental implantation may be coated with the r-laminin 5 of the invention to stimulate periodontal cell attachment. These prostheses typically comprise two separate pieces, an implant which is inserted into the bone and an abutment piece which actually contacts the junctional epithelium. Alternatively, the implant and abutment piece may be obtained as a single unit.

If the device is made of a natural or synthetic biodegradable material in the form of a mesh, sheet or fabric, the r-laminin 5 may be applied directly to the surface thereof. Epithelial cells may then be cultured on the matrix to form transplantable or implantable devices, including dental abutment pieces, needles, metal pins or rods, indwelling catheters, colostomy tubes, surgical meshes and any other appliance for which coating with the r-laminin is desirable. Alternatively, the devices may be implanted and cells may be permitted to attach in vivo. The epithelial cell-coated surgical meshes will be useful for skin allografts necessitated by compromised skin integrity.

Coupling of the r-laminin 5 may be non-covalent (such as by adsorption), or by covalent means. The device may be immersed in, incubated in, or sprayed with the r-laminin 5 of the invention. In a preferred embodiment, the concentration of r-laminin 5 for coating the device is between about 1 ng/ml and about 10 mg/ml.

The present invention also provides a method for inducing epithelial cell attachment to the device (as disclosed above), comprising coating the appliance with r-laminin 5 prior to incubation with epithelial cells.

The therapeutic application of r-laminin 5 produced in accordance with the present invention can be used for the treatment of a variety of conditions and diseases, including but not limited to Type I diabetes; skin conditions including but not limited to diabetic foot ulcers, venous ulcers, pressure sores, skin surgery, burns, acute wounds, and skin grafts; corneal ulcerations; gastro-intestinal ulcers; periodontitis; and gingivitis. The therapeutically effective amount of r-laminin 5 for use in these conditions and diseases can be readily ascertained by one of ordinary skill in the art.

The present invention may be better understood with reference to the accompanying examples that are intended for purposes of illustration only and should not be construed to limit the scope of the invention, as defined by the claims appended hereto.

15 **Examples**

Production of r-laminin-5 involved sequential transfections of a mammalian cell line with vectors containing cDNAs that encode for the chains of the laminin-5 molecule, namely $\alpha 3$, $\beta 3$ and $\gamma 2$. An additional polynucleotide sequence that encodes the 'flag' peptide (DYKDDDDK), was added to the amino terminus end of the $\beta 3$ gene to facilitate affinity purification of the expressed heterotrimeric recombinant laminin-5 molecule.

IV. Materials and Methods

Expression vector constructs for $\alpha 3$

The entire coding sequence of the $\alpha 3$ cDNA [SEQ ID NO:1] was cloned via standard techniques into the expression vector pcDNA3.1/Zeo (Invitrogen), which contains the Zeocin resistant gene for selection. The expression vectors were used to produce stable cell lines according to the manufacturer's instructions.

In order to produce a second $\alpha 3$ expression vector, the full-length $\alpha 3$ cDNA was excised from the pZeo $\alpha 3$ expression construct by digestion with KpnI-NotI restriction enzymes. The double digested $\alpha 3$ fragment was inserted in the expression vector pTarget (Promega; Madison, WI), generating pTgT $\alpha 3$. This expression construct carries the G418 resistant gene for selection of resistant clones. Both expression constructs have been analyzed by restriction enzyme mapping and DNA sequencing.

Construction of full-length $\beta 3$ chain

Two cDNA fragments, Kal5-5c and Kal92-1, each cloned into separate pCR II vectors (Invitrogen), which together encode the entire $\beta 3$ chain of laminin-5 [SEQ ID NO:19], were received from Dr. Burgeson's laboratory (4). The two fragments were cloned into a single vector to obtain the full-length $\beta 3$ chain, plasmid PCRII $\beta 3$.

Expression vector constructs for $\beta 3$

The laminin $\beta 3$ expression vector, pRCX3 $\beta 3_F$, was constructed containing the full-length $\beta 3$ chain obtained for PCRII $\beta 3$ and the FLAG epitope added to the amino terminus [SEQ ID NO:17-18]. pRCX3 is a vector derived from pRC/CMV (Invitrogen) and it contains a Geneticin resistant gene for selection with G418 sulfate, a BM 40 (SPARC) signal peptide sequence and the Flag peptide sequence in frame with convenient cloning sites

A second $\beta 3$ expression vector was constructed by excising the complete laminin $\beta 3$ -flag peptide coding region from pRCX3 $\beta 3_F$ plasmid and introducing it into pcDNA3.1/Zeo. This expression constructs carries the Zeocin resistant gene for selection.

Both $\beta 3$ -expression constructs have been analyzed by restriction enzyme mapping and DNA sequencing.

20 Expression vector constructs for $\gamma 2$

The full-length $\gamma 2$ cDNA [SEQ ID NO:29] was excised from pVL1393 $\gamma 2$ (received from Dr. Karl Tryggvason, Karolinska Institute, Sweden) by digestion with BamH I-Xba I restriction enzymes. The double digested $\gamma 2$ fragment was inserted in the corresponding sites of the expression vector pcDNA3.1/Zeo (Invitrogen), generating the pZeoy2 expression construct. This expression constructs carries the Zeocin resistant gene for selection.

Similarly, a BamH I-Not I full-length $\gamma 2$ cDNA fragment was cloned into the expression vector pTarget (Promega), generating pTgT $\gamma 2$. This expression construct carries the G418 resistant gene for selection of resistant clones.

Both expression constructs have been analyzed by restriction enzyme mapping and DNA sequencing.



Sequence analysis of expression constructs

The expression vector constructs have been sequenced and the reported gene sequences compared to the published sequences. **Table 2** shows a summary of the amino acid mismatches for the different laminin chains.

5

α3 chain: the reported sequence matched the published sequence.

10

β3 chain: several discrepancies with the published sequence were found. Single and multiple base deletions and insertions are present along the sequence. These base changes generated some silent mutations, amino acid substitutions and insertion of amino acids. These changes do not cause early termination codons. Therefore, the *β3* chain seems to be of “full-length” and the protein is being produced.

γ2 chain: This chain was reported to have 3 base changes creating 3 amino acid substitutions.

15

Table 2: Summary of amino acid differences from those reported in the literature

Laminin chain	Amino acid change
$\alpha 3$	None
$\beta 3$	P, insertion at position 251-2
	A ₃₇₂ --P ₃₇₂
	R ₄₀₈ R ₄₀₉ --Q ₄₀₈ G ₄₀₉
	R, insertion at position 421
	P ₅₈₄ —R ₅₈₄
	A ₇₉₆ —G ₇₉₆
	R ₈₉₄ S ₈₉₅ E ₈₉₆ --S ₈₉₄ E ₈₉₅ A ₈₉₆
$\gamma 2$	R ₁₆₈ —G ₁₆₈
	I ₄₇₃ —M ₄₇₃
	S ₅₂₁ —N ₅₂₁

5 Transfection of human kidney 293 cells

Wild type human kidney 293 cells were transfected with the different expression constructs utilizing standard techniques. Two transfection reagents were used, LIPOFECTAMINE™ from GIBCO (Rockville, MD) and SUPERFECT™ from Qiagen (Valencia, CA). Experiments (see below) suggested that the 293 cells do not express detectable endogenous laminin $\alpha 3$, $\beta 3$, or $\gamma 2$ chains

Briefly, both methods required mixing the transfection reagent with the DNA of interest, incubating for a brief period at room temperature, and adding the mixture to the cells. The cells were split the previous day so they were at 50-80% confluency the day of the transfection. The incubation with the DNA-reagent complexes was conducted for 2-3 hours in serum free media for LIPOFECTAMINE™ transfection or complete media for SUPERFECT™ transfection. After this incubation period the media was replaced with fresh growth media and the incubation was continued until the selection process begins.

The selection process was carried out in DMEM F12/10% FBS containing either Geneticin (G418 sulfate) at 400 $\mu\text{g/ml}$ for selection of G418 resistants, or Zeocin at 50 $\mu\text{g/ml}$ for selection of Zeocin resistants. After splitting to selective media, the cells were fed every two days with fresh selective media, until cell foci were identified. Clones transfected with the three laminin chains and secreting r-laminin 5 into the medium were selected with media containing both antibiotics.

Results

Media from human kidney 293 cells transfected with a single laminin chain were initially analyzed on Western blots using chain-specific anti-laminin-5 antibodies. Cell fractions, as well as “whole” fractions containing cells plus any deposited “matrix-like” material obtained by scraping the cells into loading buffer, were also analyzed. Western blot analysis of wild type 293 cell cultures showed no detectable laminin $\alpha 3$, $\beta 3$, or $\gamma 2$ chain proteins.

The expression of single laminin chains following transfection is generally intracellular, except for a few $\beta 3$ clones that appear to show $\beta 3$ chain reactivity in the media in Western blot analyses using the anti-FLAG antibody.

All clones showing FLAG antibody reactivity were verified by PCR to confirm the incorporation of the transfected gene. Analysis of genomic DNA preparations from such clones by PCR was done using laminin chain-specific primer pairs. The amplified products were compared to positive controls where the original expression constructs were used as templates. Results are shown in Table 3. A few selected clones were analyzed by RT-PCR using the same laminin chain-specific primers and total RNA and/or mRNA preparations as templates. These results are also shown in Table 2.

Other data (not shown) demonstrated that the molecular sizes of some of the components of r-laminin 5 were different from those in purified laminin 5. Particularly, the major component of the $\alpha 3$ chain in purified laminin 5 was 165 kD, while the $\alpha 3$ band in r-laminin 5 migrated as two chains of 150 kD and 95 kD.

Identified co-transfected clones producing all three chains (as assessed by both genomic PCR and RT-PCR analysis), were further analyzed in a keratinocyte cell adhesion binding assay.

HFK cell adhesion assay for laminin-5. The method used measures laminin-5 activity present in conditioned media from various clones. Any laminin-5 present in the test media was trapped to a 96 well via an anti-laminin $\alpha 3$ antibody (C 25). Human foreskin keratinocytes (HFK) were labeled fluorescently, added to the treated wells, and allowed to adhere for 30 minutes. Fluorescence was measured before and after washing with PBS. The % cell adhesion is equal to fraction of fluorescence retained in the well. As controls, cells were pre-incubated with an anti-integrin $\alpha 3\beta 1$ inhibitory antibody (P1B5)($\alpha 3\beta 1$ is the cell receptor for laminin 5), or non-specific control antibody (SP2)

before being added to the wells. Media controls (Keratinocyte growth media ("KGM"); or DMEM F12 culture media ("medium") were also used. The "a2_F" notation denotes culture medium from 293 cells transfected to express an unrelated FLAG-containing protein.

5 The results, shown in Table 2 (last column) and in Figure 1. The figure is labeled as follows: C5 and F10: conditioned culture media from r-laminin-5 producing clones C5 and F10; *C6 and *F10: conditioned culture media collected earlier and kept refrigerated. These data demonstrated that media from several clones produced positive results in the cell adhesion assay, indicating the r-laminin-5 produced by these clones is biologically
10 active. The activity was inhibited in the presence of an integrin $\alpha 3\beta 1$ antibody, demonstrating that the r-laminin 5 is binding to the cells via the $\alpha 3\beta 1$ integrin.

To assist in the purification of the heterotrimer r-laminin-5 molecule, the laminin $\beta 3$ chain was labeled with a 'flag' sequence at the amino terminus end. Media from clones transfected with all three chains, and shown to express all three chains, were passed
15 through an anti-flag column and eluted with excess flag peptide. The eluted fractions were analyzed by gel electrophoresis. The data demonstrate that r-laminin 5 was produced and isolated.

20 **Table 3: Summary analysis of selected r-L5 clones**

Clone	Western Blot				PCR ¹			RT-PCR ²			Adhesion Assay
	$\alpha 3$	$\beta 3$	$\gamma 2$	Flag	$\alpha 3$	$\beta 3$	$\gamma 2$	$\alpha 3$	$\beta 3$	$\gamma 2$	
A2-3	-	nd	nd	+	-	+	+	-	+	+	-
A4-3	+	+	+	+	+	+	+	+	+	+	+
A10-3	-	nd	+	+	-	+	-	-	+	+	-
B1-6	nd	nd	nd	+	+	+	+	+	+	+	+
C2-3	-	nd	+	+	-	+	+	+	+	+	-
C5-7	nd	nd	nd	+	+	+	+	nd	+	+	-
C6-3	+	+	+	+	+	+	+	+	+	+	+
C10-3	-	nd	nd	+	-	+	+	+	+	+	-
E1-3	-	nd	nd	-	-	+	-	-	+	+	-
E2-3	-	nd	+	+	-	+	-	+	+	+	-
E7-3	-	nd	-	+	-	+	-	-	+	+	-
F10-5	nd	nd	nd	+	+	+	+	+	+	+	+

nd = Not determined

1. PCR analysis of genomic DNA preparations were performed using laminin chain-specific primer pairs. The amplified products were compared to positive controls where the original expression constructs were used as templates.
25

2. RT-PCR analyses were done similarly using total RNA and/or mRNA as templates and primers as above.

Several of the above clones were selected for further analysis. A 1 liter culture from clone F10-5 was prepared, and r-laminin 5 was purified using the methods described above. The r-laminin 5 was used in an HFK cell adhesion assay exactly as described above, except that r-laminin 5 was coated directly onto the plate. The results are presented in **Figure 2** and demonstrate that r-laminin 5 markedly increases adhesion of HFK cells at all concentrations tested.

10

Electron Micrograph Analysis

Purified r-laminin 5 protein was diluted to 50 µg/ml and adjusted to 70% glycerol/30% 0.15M ammonium bicarbonate and rotary shadowed using standard techniques. **Figure 3** shows an 80,000X magnification field of (A) r-laminin 5; and (B) "native" laminin 5 (purified by BM165 monoclonal antibody affinity chromatography from SCC-25 (squamous cell carcinoma cell line) conditioned medium). The bar represents 50 nm. These results demonstrated that both the r-laminin 5 and the "native" purified laminin 5 formed similar cross-shaped structures typical of laminins.

20

The present invention is not limited by the aforementioned particular preferred embodiments. It will occur to those ordinarily skilled in the art that various modifications may be made to the disclosed preferred embodiments without diverting from the concept of the invention. All such modifications are intended to be within the scope of the present invention.

25

We claim

1. Recombinant laminin 5-expressing cells.
- 5 2. The recombinant laminin 5-expressing cells of claim 1, wherein the cells express recombinant laminin 5 comprising:
 - a first chain comprising a polypeptide that is substantially similar to an $\alpha 3$ laminin chain;
 - 10 a second chain comprising a polypeptide that is substantially similar to a $\beta 3$ laminin chain; and
 - a third chain comprising a polypeptide that is substantially similar to a $\gamma 2$ laminin chain;
 - wherein the first, second, and third chains are assembled into recombinant
 - 15 heterotrimeric laminin 5.
3. The recombinant laminin 5-expressing cells of claim 1, wherein the cells express recombinant laminin 5 comprising:
 - a first chain comprising a recombinant polypeptide that is at least 70% identical to
 - 20 one or more of SEQ ID NO:2, 4, 6, 8, 10, 12, or fragments thereof;
 - a second chain comprising a recombinant polypeptide that is at least 70% identical to one or more of SEQ ID NO:14, 16, 18, 20, 22, 24, or fragments thereof; and
 - a third chain comprising a recombinant polypeptide that is at least 70% identical to one or more of SEQ ID NO:26, 28, 30, 32, 34, 36, or fragments thereof;
 - 25 wherein the cell expresses the first, second, and third chains, and wherein the first, second, and third chains assemble into recombinant heterotrimeric laminin 5 that is secreted into the media by the cultured cell.
4. The recombinant laminin 5-expressing cells of claim 1, wherein the cells express
- 30 recombinant laminin 5 comprising:
 - a first chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO:1, 3, 5, 7, 9, 11, or fragments thereof;

a second chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO:13, 15, 17, 19, 21, 23, or fragments thereof; and

a third chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO: 25, 27, 29, 31, 33, 35, or fragments thereof;

wherein the cell expresses the first, second, and third chains, and wherein the first, second, and third chains assemble into recombinant heterotrimeric laminin 5 that is secreted into the media by the cultured cell.

10

5. The recombinant laminin 5-expressing host cells of claim 1, wherein the cells express recombinant laminin 5 comprising a first, second, and third polypeptide chain, wherein the first, second, and third polypeptide chains each comprise a general structure selected from the group consisting of: (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e)

15

wherein R1 is a amino terminal methionine; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, or it may be an artificial sequence; R3 is a secreted $\alpha 3$ laminin chain for the first polypeptide chain, a secreted $\beta 3$ laminin chain for the second polypeptide chain, and $\gamma 2$ laminin chain for the third polypeptide chain; and R3(e) is identical to R3, but further comprises an epitope tag .

20

6. A method of purifying recombinant laminin 5, comprising:

- a. providing the eukaryotic cells of any one of claim 1-5;
- 25 b. growing the cells in cell culture medium under conditions to stimulate expression of the recombinant laminin 5 chains;
- c. passing the cell culture medium through an affinity chromatography column, wherein the column contains a compound that specifically binds to the epitope tag;
- 30 d. washing the affinity column to remove unbound materials; and
- e. eluting the bound recombinant laminin 5 from the column.

7. Purified recombinant laminin 5 isolated according to the method of claim 6.
8. Purified recombinant laminin 5.
- 5
9. The substantially purified recombinant laminin 5 of claim 8 comprising:
a first chain comprising a polypeptide that is substantially similar to an $\alpha 3$ laminin chain;
a second chain comprising a polypeptide that is substantially similar to a $\beta 3$
10 laminin chain; and
a third chain comprising a polypeptide that is substantially similar to a $\gamma 2$ laminin chain;
wherein the first, second, and third chains are assembled into recombinant heterotrimeric laminin 5.
- 15
10. The purified recombinant laminin 5 of claim 8, comprising:
a first chain comprising a recombinant polypeptide that is at least 70% identical to one or more of SEQ ID NO:2, 4, 6, 8, 10, 12, or fragments thereof;
a second chain comprising a recombinant polypeptide that is at least 70% identical
20 to one or more of SEQ ID NO:14, 16, 18, 20, 22, 24, or fragments thereof; and
a third chain comprising a recombinant polypeptide that is at least 70% identical to one or more of SEQ ID NO:26, 28, 30, 32, 34, 36, or fragments thereof;
wherein the first, second, and third chains are assembled into recombinant heterotrimeric laminin 5.
- 25
11. The purified recombinant laminin 5 of claim 8, comprising:
a first chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO:1, 3, 5, 7, 9, 11, or fragments thereof;
30 a second chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO:13, 15, 17, 19, 21, 23, or fragments thereof; and

a third chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of SEQ ID NO: 25, 27, 29, 31, 33, 35, or fragments thereof; wherein the first, second, and third chains are assembled into recombinant heterotrimeric laminin 5.

5

12. The purified recombinant heterotrimeric laminin 5 of claim 8, comprising a first, second, and third polypeptide chain, wherein the first, second, and third polypeptide chains each comprise a general structure selected from the group consisting of: (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-
10 R3(e)

wherein R1 is a amino terminal methionine; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, or it may be an artificial sequence; R3 is a secreted $\alpha 3$ laminin chain for the first polypeptide chain,
15 a secreted $\beta 3$ laminin chain for the second polypeptide chain, and a secreted $\gamma 2$ laminin chain for the third polypeptide chain; and R3(e) is identical to R3, but further comprises an epitope tag.

13. A pharmaceutical composition comprising:
20 a. the recombinant laminin 5 of any of claims 7-12; and
b. a pharmaceutically acceptable carrier.

14. A method for accelerating wound healing comprising administering to a patient in need thereof an amount effective of the recombinant laminin 5 of any of claims 7-12 to
25 accelerate wound healing.

15. The method of claim 14 wherein the wound is selected from the group consisting of diabetic foot ulcers, venous ulcers, pressure sores, skin surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-intestinal ulcers, periodontitis, and gingivitis.

30 16. A method to improve the biocompatibility of a medical device, comprising contacting the medical device with an amount effective of the recombinant laminin 5 of any of claims 7-12 to improve the biocompatibility of the medical device.

17. A method to promote cell adhesion to a surface, comprising contacting the cells with an amount effective of the recombinant laminin 5 of any of claims 7-12 to promote cell adhesion to a surface.

5

18. An improved method for the ex vivo treatment of Type I diabetes in a patient in need thereof, wherein the improvement consists of culturing isolated pancreatic islet beta in the presence of an amount effective the recombinant laminin 5 of any of claims 7-12 to promote adhesion of the pancreatic islet beta cells to a surface, culturing the cells, and re-
10 introducing the cells into the patient.

19. A method for regulating angiogenesis, comprising contacting a tissue in need thereof with an amount effective to promote angiogenesis of laminin 5 to regulate angiogenesis.

15

20. The method of claim 19, wherein the laminin 5 comprises recombinant laminin 5 according to any one of claims 7-12.

21. An improved cell growth substrate, wherein the improvement consists of providing
20 a cell growth substrate that has been coated with an amount effective of the recombinant laminin 5 of any of claims 7-12 to promote cell attachment to the cell growth substrate.

22. An improved cell culture medium, wherein the improvement consists of providing an amount effective of the recombinant laminin 5 of any of claims 7-12 to promote cell
25 attachment to a cell growth substrate.

23. An improved medical implantation device, wherein the improvement consists of providing a medical implantation device that has been coated with an amount effective of the recombinant laminin 5 of any of claims 7-12 to promote cell attachment to the medical
30 implantation device.

24. The improved medical implantation device of claim 23, wherein the medical implantation device is selected from the group consisting of artificial grafts, indwelling or transcutaneous catheter, polytetrafluoroethylene, expanded polytetrafluoroethylene, needle, metal pin, metal rod, colostomy tube, transcutaneous catheter, dental abutment
5 piece or surgical mesh.

25. A method for accelerating wound healing comprising administering to a patient in need thereof an amount effective of the pharmaceutical composition of claim 13 to accelerate wound healing.

10

26. The method of claim 25 wherein the wound is selected from the group consisting of diabetic foot ulcers, venous ulcers, pressure sores, skin surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-intestinal ulcers, periodontitis, and gingivitis.

15 27. A method to improve the biocompatibility of a medical device, comprising contacting the medical device with an amount effective of the pharmaceutical composition of claim 13 to improve the biocompatibility of the medical device.

20 28. A method to promote cell adhesion to a surface, comprising contacting the cells with an amount effective of the pharmaceutical composition of claim 13 to promote cell adhesion to a surface.

25 29. An improved method for the ex vivo treatment of Type I diabetes in a patient in need thereof, wherein the improvement consists of culturing isolated pancreatic islet beta in the presence of an amount effective the pharmaceutical composition of claim 13 to promote adhesion of the pancreatic islet beta cells to a surface, culturing the cells, and re-introducing the cells into the patient.

30 30. A method for regulating angiogenesis, comprising contacting a tissue in need thereof with an amount effective to regulate angiogenesis of the pharmaceutical composition of claim 13 to regulate angiogenesis.

31. An improved cell growth substrate, wherein the improvement consists of providing a cell growth substrate that has been coated with an amount effective of the pharmaceutical composition of claim 13 to promote cell attachment to the cell growth substrate.

5

32. An improved medical implantation device, wherein the improvement consists of providing a medical implantation device that has been coated with an amount effective of the pharmaceutical composition of claim 13 to promote cell attachment to the medical implantation device.

10

33. The improved medical implantation device of claim 32, wherein the medical implantation device is selected from the group consisting of artificial grafts, indwelling or transcutaneous catheter, polytetrafluoroethylene, expanded polytetrafluoroethylene, needle, metal pin, metal rod, colostomy tube, transcutaneous catheter, dental abutment piece or surgical mesh.

15

34. An isolated polynucleotide sequence selected from the group consisting of SEQ ID 21, SEQ ID NO:23, SEQ ID NO:29, SEQ ID NO:31.

20

35. An isolated polypeptide sequence selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:30, and SEQ ID NO:32.

FIG. 1

Figure 1 : HFK cell adhesion assay

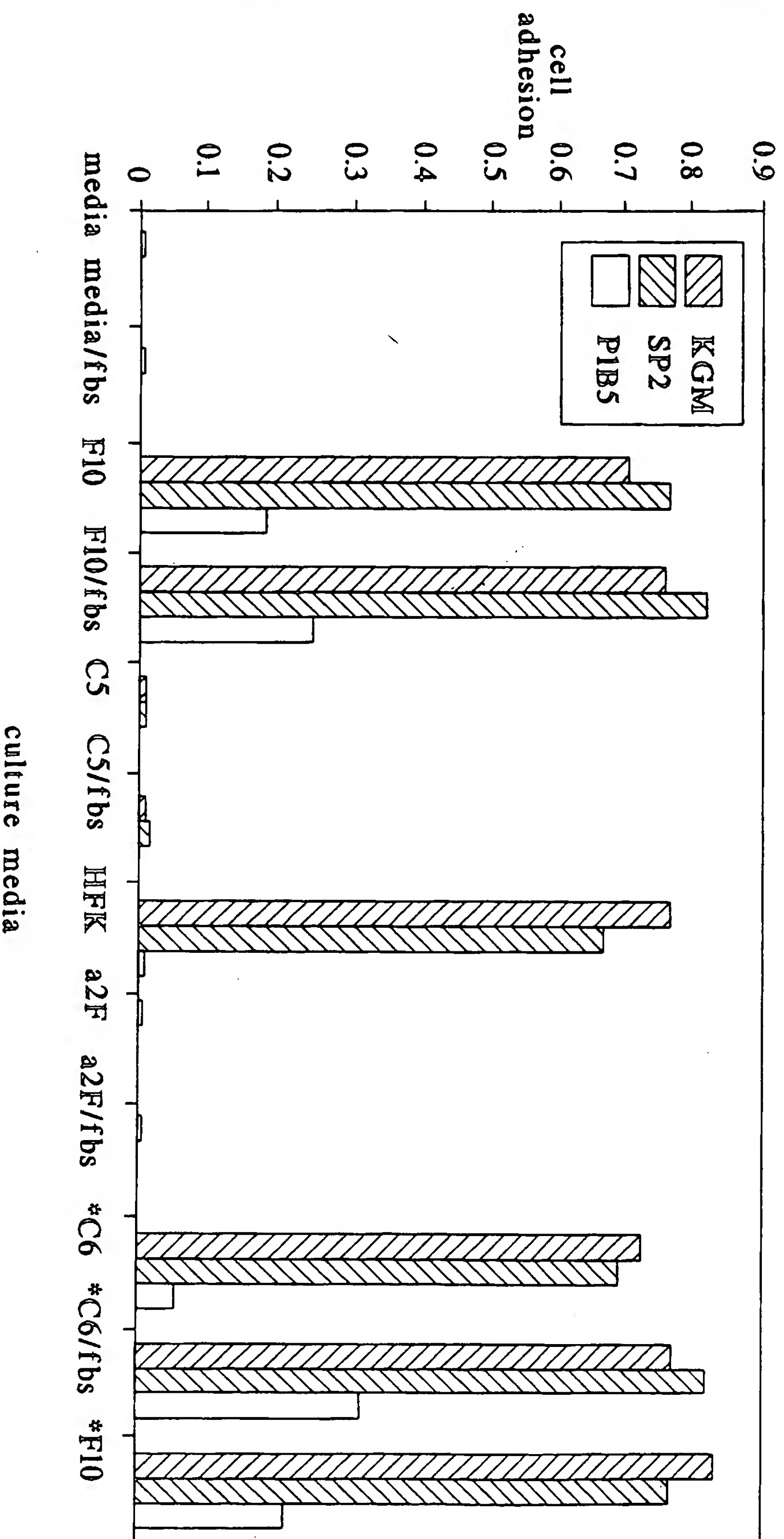


FIG. 2
HEK adhesion to purified r-laminin 5

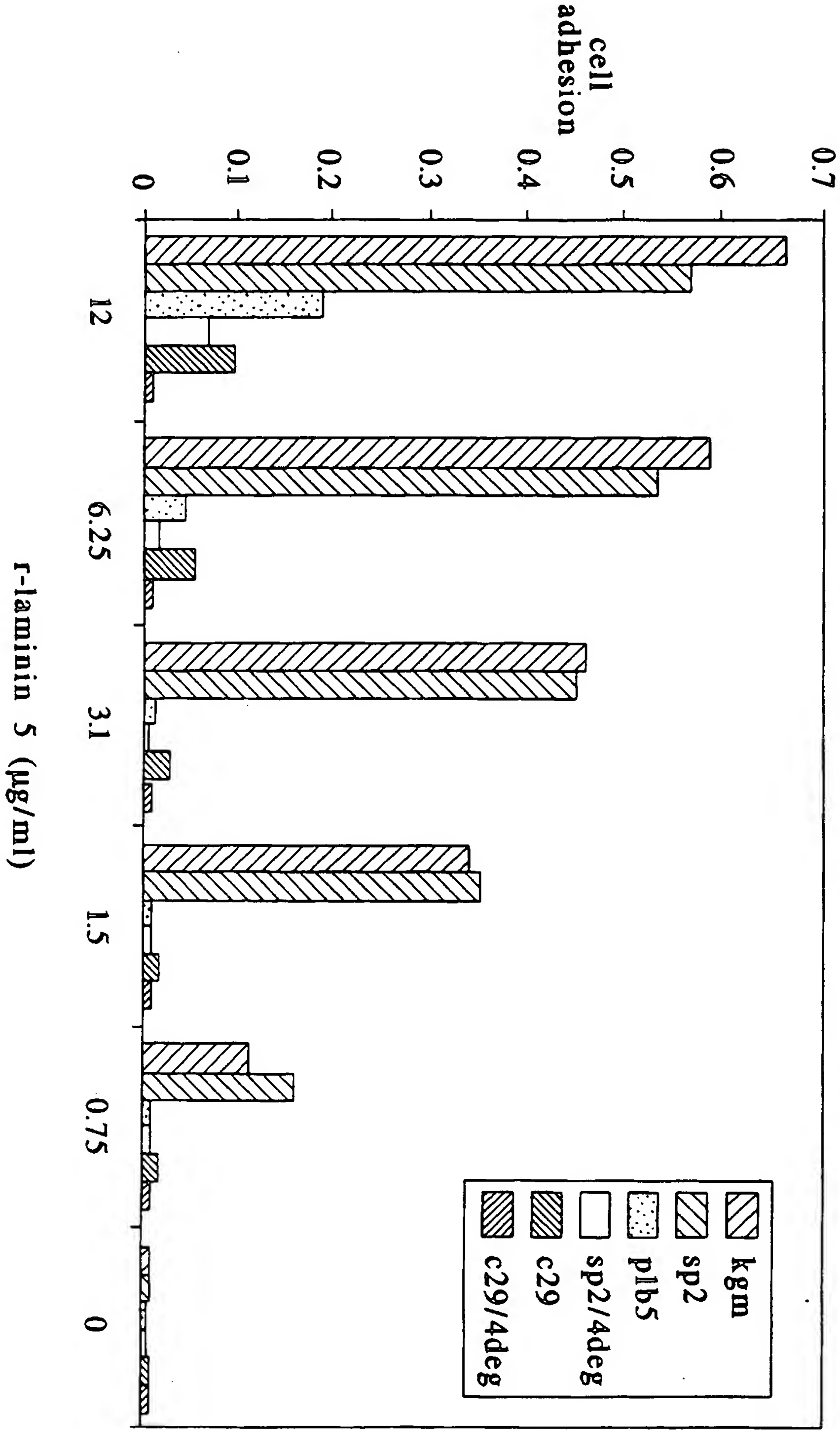
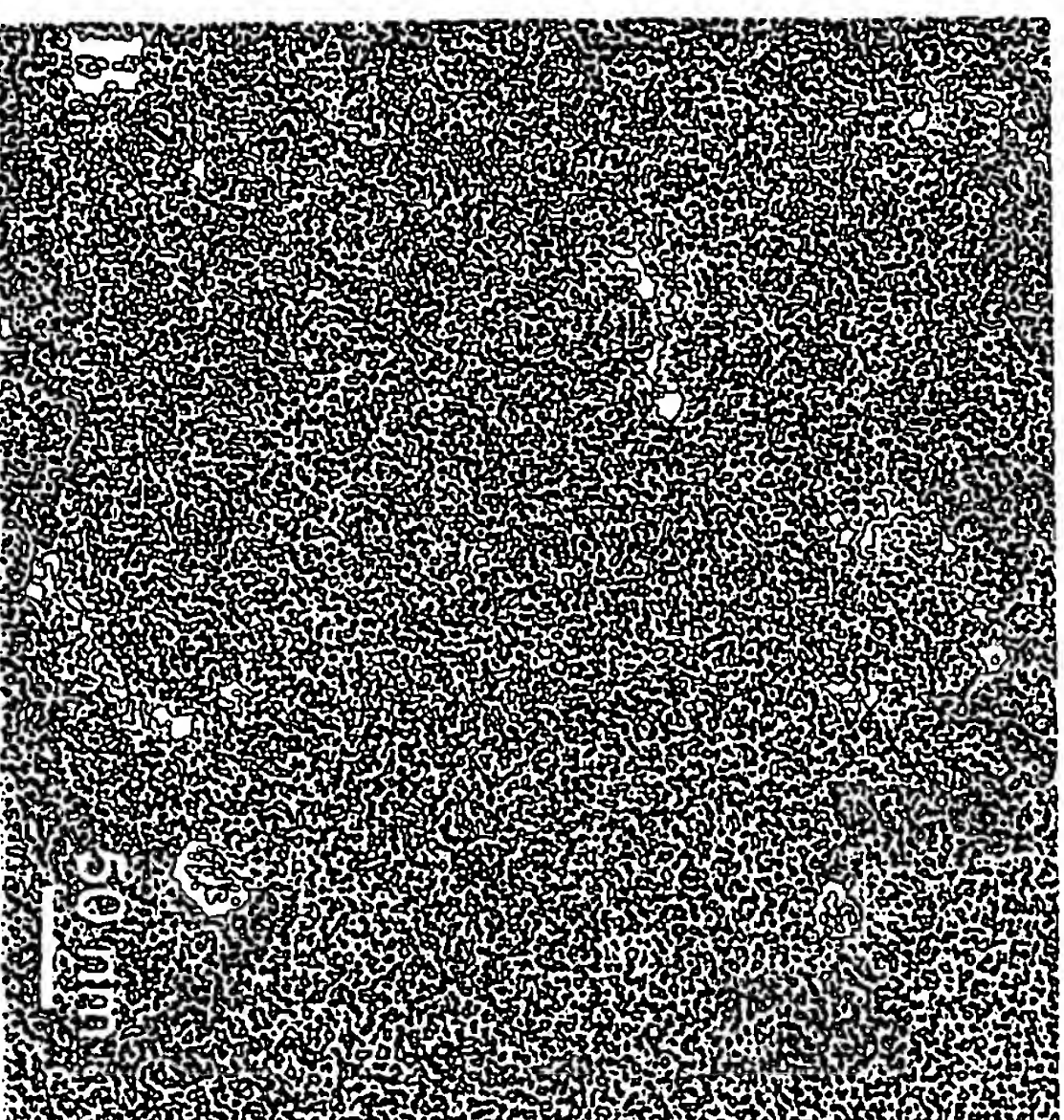
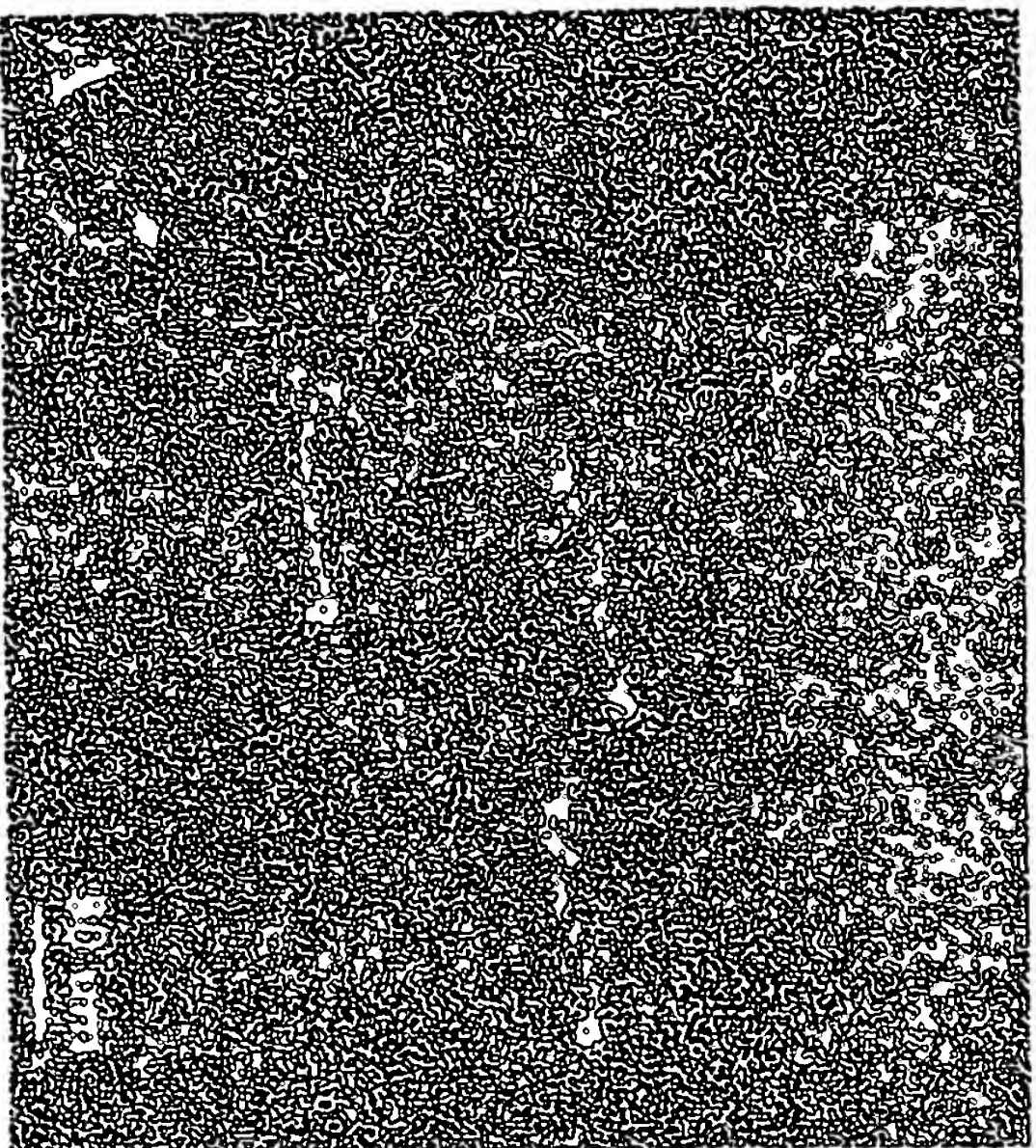


Figure 3

Rotary-shadowed electron micrographs of
recombinant laminin 5 (A) and “native” laminin 5 (B).



SEQUENCE LISTING

<110> Boutand, Ariel

<120> Recombinant Laminin 5

<130> 99-274-C1

<140> To Be Assigned

<141> Filed Herewith

<160> 36

<170> PatentIn Ver. 2.0

<210> 1

<211> 5280

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18)..(5189)

<220>

<221> sig_peptide

<222> (18)..(110)

<400> 1

taattaactg gttccgg atg cct cca gca gtg agg cgg tca gcc tgc agc	50
Met Pro Pro Ala Val Arg Arg Ser Ala Cys Ser	
1 5 10	
atg gga tgg ctg tgg atc ttt ggg gca gcc ctg ggg cag tgt ctg ggc	98
Met Gly Trp Leu Trp Ile Phe Gly Ala Ala Leu Gly Gln Cys Leu Gly	
15 20 25	
tac agt tca cag cag caa agg gtg cca ttt ctt cag cct ccc ggt caa	146
Tyr Ser Ser Gln Gln Gln Arg Val Pro Phe Leu Gln Pro Pro Gly Gln	
30 35 40	
agt caa ctg caa gcg agt tat gtg gag ttt aga ccc agc cag ggt tgt	194
Ser Gln Leu Gln Ala Ser Tyr Val Glu Phe Arg Pro Ser Gln Gly Cys	
45 50 55	
agc cct gga tac tat cgg gat cat aaa ggc ttg tat acc gga cgg tgt	242
Ser Pro Gly Tyr Tyr Arg Asp His Lys Gly Leu Tyr Thr Gly Arg Cys	
60 65 70 75	
gtt ccc tgc aat tgc aac gga cat tca aat caa tgc cag gat ggc tca	290
Val Pro Cys Asn Cys Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser	
80 85 90	
ggc ata tgt gtt aac tgt cag cac aac acc gcg gga gag cac tgt gaa	338
Gly Ile Cys Val Asn Cys Gln His Asn Thr Ala Gly Glu His Cys Glu	
95 100 105	
cgc tgc cag gag ggc tac tat ggc aac gcc gtc cac gga tcc tgc agg	386
Arg Cys Gln Glu Gly Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg	
110 115 120	

gcc tgc cca tgt cct cac act aac agc ttt gcc act ggc tgt gtg gtg	434
Ala Cys Pro Cys Pro His Thr Asn Ser Phe Ala Thr Gly Cys Val Val	
125 130 135	
aat ggg gga gac gtg cgg tgc tcc tgc aaa gct ggg tac aca gga aca	482
Asn Gly Gly Asp Val Arg Cys Ser Cys Lys Ala Gly Tyr Thr Gly Thr	
140 145 150 155	
cag tgt gaa agg tgt gca ccg gga tat ttc ggg aat ccc cag aaa ttc	530
Gln Cys Glu Arg Cys Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe	
160 165 170	
gga ggt agc tgc caa cca tgc agt tgt aac agc aat ggc cag ctg ggc	578
Gly Gly Ser Cys Gln Pro Cys Ser Cys Asn Ser Asn Gly Gln Leu Gly	
175 180 185	
agc tgt cat ccc ctg act gga gac tgc ata aac caa gaa ccc aaa gat	626
Ser Cys His Pro Leu Thr Gly Asp Cys Ile Asn Gln Glu Pro Lys Asp	
190 195 200	
agc agc cct gca gaa gaa tgt gat gat tgc gac agc tgt gtg atg acc	674
Ser Ser Pro Ala Glu Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr	
205 210 215	
ctc ctg aac gac ctg gcc acc atg ggc gag cag ctc cgc ctg gtc aag	722
Leu Leu Asn Asp Leu Ala Thr Met Gly Glu Gln Leu Arg Leu Val Lys	
220 225 230 235	
tct cag ctg cag ggc ctg agt gcc agc gca ggg ctt ctg gag cag atg	770
Ser Gln Leu Gln Gly Leu Ser Ala Ser Ala Gly Leu Leu Glu Gln Met	
240 245 250	
agg cac atg gag acc cag gcc aag gac ctg agg aat cag ttg ctc aac	818
Arg His Met Glu Thr Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Asn	
255 260 265	
tac cgt tct gcc att tca aat cat gga tca aaa ata gaa ggc ctg gaa	866
Tyr Arg Ser Ala Ile Ser Asn His Gly Ser Lys Ile Glu Gly Leu Glu	
270 275 280	
aga gaa ctg act gat ttg aat caa gaa ttt gag act tta caa gaa aag	914
Arg Glu Leu Thr Asp Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys	
285 290 295	
gct caa gta aat tcc aga aaa gca caa aca tta aac aac aat gtt aat	962
Ala Gln Val Asn Ser Arg Lys Ala Gln Thr Leu Asn Asn Asn Val Asn	
300 305 310 315	
cgg gca aca caa agc gca aaa gaa cta gat gtg aag att aaa aat gtc	1010
Arg Ala Thr Gln Ser Ala Lys Glu Leu Asp Val Lys Ile Lys Asn Val	
320 325 330	
atc cgg aat gtg cac att ctt tta aag cag atc tct ggg aca gat gga	1058
Ile Arg Asn Val His Ile Leu Leu Lys Gln Ile Ser Gly Thr Asp Gly	
335 340 345	
gag gga aac aac gtg cct tca ggt gac ttt tcc aga gag tgg gct gaa	1106
Glu Gly Asn Asn Val Pro Ser Gly Asp Phe Ser Arg Glu Trp Ala Glu	
350 355 360	
gcc cag cgc atg atg agg gaa ctg cgg aac agg aac ttt gga aag cac	1154

Ala	Gln	Arg	Met	Met	Arg	Glu	Leu	Arg	Asn	Arg	Asn	Phe	Gly	Lys	His		
365						370					375						
ctc	aga	gaa	gca	gaa	gct	gat	aaa	agg	gag	tcg	cag	ctc	ttg	ctg	aac	1202	
Leu	Arg	Glu	Ala	Glu	Ala	Asp	Lys	Arg	Glu	Ser	Gln	Leu	Leu	Leu	Asn		
380					385					390					395		
cgg	ata	agg	acc	tgg	cag	aaa	acc	cac	cag	ggg	gag	aac	aat	ggg	ctt	1250	
Arg	Ile	Arg	Thr	Trp	Gln	Lys	Thr	His	Gln	Gly	Glu	Asn	Asn	Gly	Leu		
				400					405					410			
gct	aac	agt	atc	cgg	gat	tct	tta	aat	gaa	tac	gaa	gcc	aaa	ctc	agt	1298	
Ala	Asn	Ser	Ile	Arg	Asp	Ser	Leu	Asn	Glu	Tyr	Glu	Ala	Lys	Leu	Ser		
			415					420					425				
gac	ctt	cgt	gct	cgg	ctg	cag	gag	gca	gct	gcc	caa	gcc	aag	cag	gca	1346	
Asp	Leu	Arg	Ala	Arg	Leu	Gln	Glu	Ala	Ala	Ala	Gln	Ala	Lys	Gln	Ala		
			430				435					440					
aat	ggc	ttg	aac	caa	gaa	aac	gag	aga	gct	ttg	gga	gcc	att	cag	aga	1394	
Asn	Gly	Leu	Asn	Gln	Glu	Asn	Glu	Arg	Ala	Leu	Gly	Ala	Ile	Gln	Arg		
	445					450					455						
caa	gtg	aaa	gaa	ata	aat	tcc	ctg	cag	agt	gat	ttc	acc	aag	tat	cta	1442	
Gln	Val	Lys	Glu	Ile	Asn	Ser	Leu	Gln	Ser	Asp	Phe	Thr	Lys	Tyr	Leu		
460					465					470					475		
acc	act	gca	gac	tca	tct	ttg	ttg	caa	acc	aac	att	gcg	ctg	cag	ctg	1490	
Thr	Thr	Ala	Asp	Ser	Ser	Leu	Leu	Gln	Thr	Asn	Ile	Ala	Leu	Gln	Leu		
				480					485					490			
atg	gag	aaa	agc	cag	aag	gaa	tat	gaa	aaa	tta	gct	gcc	agt	tta	aat	1538	
Met	Glu	Lys	Ser	Gln	Lys	Glu	Tyr	Glu	Lys	Leu	Ala	Ala	Ser	Leu	Asn		
			495					500					505				
gaa	gca	aga	caa	gaa	cta	agt	gac	aaa	gta	aga	gaa	ctt	tcc	aga	tct	1586	
Glu	Ala	Arg	Gln	Glu	Leu	Ser	Asp	Lys	Val	Arg	Glu	Leu	Ser	Arg	Ser		
			510				515					520					
gct	ggc	aaa	aca	tcc	ctt	gtg	gag	gag	gca	gaa	aag	cac	gcg	cgg	tcc	1634	
Ala	Gly	Lys	Thr	Ser	Leu	Val	Glu	Glu	Ala	Glu	Lys	His	Ala	Arg	Ser		
	525					530					535						
tta	caa	gag	ctg	gca	aag	cag	ctg	gaa	gag	atc	aag	aga	aac	gcc	agc	1682	
Leu	Gln	Glu	Leu	Ala	Lys	Gln	Leu	Glu	Glu	Ile	Lys	Arg	Asn	Ala	Ser		
540					545					550					555		
ggg	gat	gag	ctg	gtg	cgc	tgt	gct	gtg	gat	gcc	gcc	acc	gcc	tac	gag	1730	
Gly	Asp	Glu	Leu	Val	Arg	Cys	Ala	Val	Asp	Ala	Ala	Thr	Ala	Tyr	Glu		
				560				565						570			
aac	atc	ctc	aat	gcc	atc	aaa	gcg	gcc	gag	gac	gca	gcc	aac	agg	gct	1778	
Asn	Ile	Leu	Asn	Ala	Ile	Lys	Ala	Ala	Glu	Asp	Ala	Ala	Asn	Arg	Ala		
			575					580					585				
gcc	agt	gca	tct	gaa	tct	gcc	ctc	cag	aca	gtg	ata	aag	gaa	gat	ctg	1826	
Ala	Ser	Ala	Ser	Glu	Ser	Ala	Leu	Gln	Thr	Val	Ile	Lys	Glu	Asp	Leu		
			590				595					600					
cca	aga	aaa	gct	aaa	acc	ctg	agt	tcc	aac	agt	gat	aaa	ctg	tta	aat	1874	
Pro	Arg	Lys	Ala	Lys	Thr	Leu	Ser	Ser	Asn	Ser	Asp	Lys	Leu	Leu	Asn		

605	610	615	
gaa gcc aag atg aca caa aag aag cta aag caa gaa gtc agt cca gct Glu Ala Lys Met Thr Gln Lys Lys Leu Lys Gln Glu Val Ser Pro Ala 620 625 630 635			1922
ctc aac aac cta cag caa acc ctg aat att gtg aca gtt cag aaa gaa Leu Asn Asn Leu Gln Gln Thr Leu Asn Ile Val Thr Val Gln Lys Glu 640 645 650			1970
gtg ata gac acc aat ctc aca act ctc cga gat ggt ctt cat ggg ata Val Ile Asp Thr Asn Leu Thr Thr Leu Arg Asp Gly Leu His Gly Ile 655 660 665			2018
cag aga ggt gat att gat gct atg atc agt agt gca aag agc atg gtc Gln Arg Gly Asp Ile Asp Ala Met Ile Ser Ser Ala Lys Ser Met Val 670 675 680			2066
aga aag gcc aac gac atc aca gat gag gtt ctg gat ggg ctc aac ccc Arg Lys Ala Asn Asp Ile Thr Asp Glu Val Leu Asp Gly Leu Asn Pro 685 690 695			2114
atc cag aca gat gtg gaa aga att aag gac acc tat ggg agg aca cag Ile Gln Thr Asp Val Glu Arg Ile Lys Asp Thr Tyr Gly Arg Thr Gln 700 705 710 715			2162
aac gaa gac ttc aaa aag gct ctg act gat gca gat aac tcg gtg aat Asn Glu Asp Phe Lys Lys Ala Leu Thr Asp Ala Asp Asn Ser Val Asn 720 725 730			2210
aag tta acc aac aaa cta cct gat ctt tgg cgc aag att gaa agt atc Lys Leu Thr Asn Lys Leu Pro Asp Leu Trp Arg Lys Ile Glu Ser Ile 735 740 745			2258
aac caa cag ctg ttg ccc ttg gga aac atc tct gac aac atg gac aga Asn Gln Gln Leu Leu Pro Leu Gly Asn Ile Ser Asp Asn Met Asp Arg 750 755 760			2306
ata cga gaa cta att cag cag gcc aga gat gct gcc agt aag gtt gct Ile Arg Glu Leu Ile Gln Gln Ala Arg Asp Ala Ala Ser Lys Val Ala 765 770 775			2354
gtc ccc atg agg ttc aat ggt aaa tct gga gtc gaa gtc cga ctg cca Val Pro Met Arg Phe Asn Gly Lys Ser Gly Val Glu Val Arg Leu Pro 780 785 790 795			2402
aat gac ctg gaa gat ttg aaa gga tat aca tct ctg tcc ttg ttt ctc Asn Asp Leu Glu Asp Leu Lys Gly Tyr Thr Ser Leu Ser Leu Phe Leu 800 805 810			2450
caa agg ccc aac tca aga gaa aat ggg ggt act gag aat atg ttt gtg Gln Arg Pro Asn Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val 815 820 825			2498
atg tac ctt gga aat aaa gat gcc tcc cgg gac tac atc ggc atg gca Met Tyr Leu Gly Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala 830 835 840			2546
gtt gtg gat ggc cag ctc acc tgt gtc tac aac ctg ggg gac cgt gag Val Val Asp Gly Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu 845 850 855			2594

gct gaa ctc caa gtg gac cag atc ttg acc aag agt gag act aag gag	2642
Ala Glu Leu Gln Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu	
860 865 870 875	
gca gtt atg gat cgg gtg aaa ttt cag aga att tat cag ttt gca agg	2690
Ala Val Met Asp Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg	
880 885 890	
ctt aat tac acc aaa gga gcc aca tcc agt aaa cca gaa aca ccc gga	2738
Leu Asn Tyr Thr Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly	
895 900 905	
gtc tat gac atg gat ggt aga aat agc aat aca ctc ctt aat ttg gat	2786
Val Tyr Asp Met Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp	
910 915 920	
cct gaa aat gtt gta ttt tat gtt gga ggt tac cca cct gat ttt aaa	2834
Pro Glu Asn Val Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys	
925 930 935	
ctt ccc agt cga cta agt ttc cct cca tac aaa ggt tgt att gaa tta	2882
Leu Pro Ser Arg Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu	
940 945 950 955	
gat gac ctc aat gaa aat gtt ctg agc ttg tac aac ttc aaa aaa aca	2930
Asp Asp Leu Asn Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr	
960 965 970	
ttc aat ctc aac aca act gaa gtg gag cct tgt aga agg agg aag gaa	2978
Phe Asn Leu Asn Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu	
975 980 985	
gag tca gac aaa aat tat ttt gaa ggt acg ggc tat gct cga gtt cca	3026
Glu Ser Asp Lys Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro	
990 995 1000	
act caa cca cat gct ccc atc cca acc ttt gga cag aca att cag acc	3074
Thr Gln Pro His Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr	
1005 1010 1015	
acc gtg gat aga ggc ttg ctg ttc ttt gca gaa aac ggg gat cgc ttc	3122
Thr Val Asp Arg Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe	
1020 1025 1030 1035	
ata tct cta aat ata gaa gat ggc aag ctc atg gtg aga tac aaa ctg	3170
Ile Ser Leu Asn Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu	
1040 1045 1050	
aat tca gag cta cca aaa gag aga gga gtt gga gac gcc ata aac aac	3218
Asn Ser Glu Leu Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn	
1055 1060 1065	
ggc aga gac cat tcg att cag atc aaa att gga aaa ctc caa aag cgt	3266
Gly Arg Asp His Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg	
1070 1075 1080	
atg tgg ata aat gtg gac gtt caa aac act ata att gat ggt gaa gta	3314
Met Trp Ile Asn Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val	
1085 1090 1095	

ttt gat ttc agc aca tat tat ctg gga gga att cca att gca atc agg	3362
Phe Asp Phe Ser Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg	
1100 1105 1110 1115	
gaa aga ttt aac att tct acg cct gct ttc cga ggc tgc atg aaa aat	3410
Glu Arg Phe Asn Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn	
1120 1125 1130	
ttg aag aaa acc agt ggt gtc gtt aga ttg aat gat act gtg gga gta	3458
Leu Lys Lys Thr Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val	
1135 1140 1145	
acc aaa aag tgc tcg gaa gac tgg aag ctt gtg cga tct gcc tca ttc	3506
Thr Lys Lys Cys Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe	
1150 1155 1160	
tcc aga gga gga caa ttg agt ttc act gat ttg ggc tta cca cct act	3554
Ser Arg Gly Gly Gln Leu Ser Phe Thr Asp Leu Gly Leu Pro Pro Thr	
1165 1170 1175	
gac cac ctc cag gcc tca ttt gga ttt cag acc ttt caa ccc agt ggc	3602
Asp His Leu Gln Ala Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly	
1180 1185 1190 1195	
ata tta tta gat cat cag aca tgg aca agg aac ctg cag gtc act ctg	3650
Ile Leu Leu Asp His Gln Thr Trp Thr Arg Asn Leu Gln Val Thr Leu	
1200 1205 1210	
gaa gat ggt tac att gaa ttg agc acc agc gat agc ggc ggc cca att	3698
Glu Asp Gly Tyr Ile Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile	
1215 1220 1225	
ttt aaa tct cca cag acg tat atg gat ggt tta ctg cat tat gta tct	3746
Phe Lys Ser Pro Gln Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser	
1230 1235 1240	
gta ata agc gac aac tct gga cta cgg ctt ctc atc gat gac cag ctt	3794
Val Ile Ser Asp Asn Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu	
1245 1250 1255	
ctg aga aat agc aaa agg cta aaa cac att tca agt tcc cgg cag tct	3842
Leu Arg Asn Ser Lys Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser	
1260 1265 1270 1275	
ctg cgt ctg ggc ggg agc aat ttt gag ggt tgt att agc aat gtt ttt	3890
Leu Arg Leu Gly Gly Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe	
1280 1285 1290	
gtc cag agg tta tca ctg agt cct gaa gtc cta gat ttg acc agt aac	3938
Val Gln Arg Leu Ser Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn	
1295 1300 1305	
tct ctc aag aga gat gtg tcc ctg gga ggc tgc agt tta aac aaa cca	3986
Ser Leu Lys Arg Asp Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro	
1310 1315 1320	
cct ttt cta atg ttg ctt aaa ggt tct acc agg ttt aac aag acc aag	4034
Pro Phe Leu Met Leu Leu Lys Gly Ser Thr Arg Ph Asn Lys Thr Lys	
1325 1330 1335	
act ttt cgt atc aac cag ctg ttg cag gac aca cca gtg gcc tcc cca	4082

7

1580	1585	1590	1595	
cac tta tgt gtt tac ctg gag gca gga aag gtc acg gcc tct atg gac				4850
His Leu Cys Val Tyr Leu Glu Ala Gly Lys Val Thr Ala Ser Met Asp				
	1600	1605	1610	
agt ggg gca ggt ggg acc tca acg tcg gtc aca cca aag cag tct ctg				4898
Ser Gly Ala Gly Gly Thr Ser Thr Ser Val Thr Pro Lys Gln Ser Leu				
	1615	1620	1625	
tgt gat gga cag tgg cac tcg gtg gca gtc acc ata aaa caa cac atc				4946
Cys Asp Gly Gln Trp His Ser Val Ala Val Thr Ile Lys Gln His Ile				
	1630	1635	1640	
ctg cac ctg gaa ctg gac aca gac agt agc tac aca gct gga cag atc				4994
Leu His Leu Glu Leu Asp Thr Asp Ser Ser Tyr Thr Ala Gly Gln Ile				
	1645	1650	1655	
ccc ttc cca cct gcc agc act caa gag cca cta cac ctt gga ggt gct				5042
Pro Phe Pro Pro Ala Ser Thr Gln Glu Pro Leu His Leu Gly Gly Ala				
	1660	1665	1670	1675
cca gcc aat ttg acg aca ctg agg atc cct gtg tgg aaa tca ttc ttt				5090
Pro Ala Asn Leu Thr Thr Leu Arg Ile Pro Val Trp Lys Ser Phe Phe				
	1680	1685	1690	
ggc tgt ctg agg aat att cat gtc aat cac atc cct gtc cct gtc act				5138
Gly Cys Leu Arg Asn Ile His Val Asn His Ile Pro Val Pro Val Thr				
	1695	1700	1705	
gaa gcc ttg gaa gtc cag ggg cct gtc agt ctg aat ggt tgt cct gac				5186
Glu Ala Leu Glu Val Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp				
	1710	1715	1720	
cag taaccaagc ctatttcaca gcaaggaaat tcaccttcaa aagcactgat				5239
Gln				
taccaaatgc acctccctcc ccagctcgag atcattcttc a				5280

<210> 2
 <211> 1724
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Pro Pro Ala Val Arg Arg Ser Ala Cys Ser Met Gly Trp Leu Trp
 1 5 10 15
 Ile Phe Gly Ala Ala Leu Gly Gln Cys Leu Gly Tyr Ser Ser Gln Gln
 20 25 30
 Gln Arg Val Pro Phe Leu Gln Pro Pro Gly Gln Ser Gln Leu Gln Ala
 35 40 45
 Ser Tyr Val Glu Phe Arg Pro Ser Gln Gly Cys Ser Pro Gly Tyr Tyr
 50 55 60
 Arg Asp His Lys Gly Leu Tyr Thr Gly Arg Cys Val Pro Cys Asn Cys
 65 70 75 80

Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser Gly Ile Cys Val Asn
85 90 95

Cys Gln His Asn Thr Ala Gly Glu His Cys Glu Arg Cys Gln Glu Gly
100 105 110

Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg Ala Cys Pro Cys Pro
115 120 125

His Thr Asn Ser Phe Ala Thr Gly Cys Val Val Asn Gly Gly Asp Val
130 135 140

Arg Cys Ser Cys Lys Ala Gly Tyr Thr Gly Thr Gln Cys Glu Arg Cys
145 150 155 160

Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe Gly Gly Ser Cys Gln
165 170 175

Pro Cys Ser Cys Asn Ser Asn Gly Gln Leu Gly Ser Cys His Pro Leu
180 185 190

Thr Gly Asp Cys Ile Asn Gln Glu Pro Lys Asp Ser Ser Pro Ala Glu
195 200 205

Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr Leu Leu Asn Asp Leu
210 215 220

Ala Thr Met Gly Glu Gln Leu Arg Leu Val Lys Ser Gln Leu Gln Gly
225 230 235 240

Leu Ser Ala Ser Ala Gly Leu Leu Glu Gln Met Arg His Met Glu Thr
245 250 255

Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Asn Tyr Arg Ser Ala Ile
260 265 270

Ser Asn His Gly Ser Lys Ile Glu Gly Leu Glu Arg Glu Leu Thr Asp
275 280 285

Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys Ala Gln Val Asn Ser
290 295 300

Arg Lys Ala Gln Thr Leu Asn Asn Asn Val Asn Arg Ala Thr Gln Ser
305 310 315 320

Ala Lys Glu Leu Asp Val Lys Ile Lys Asn Val Ile Arg Asn Val His
325 330 335

Ile Leu Leu Lys Gln Ile Ser Gly Thr Asp Gly Glu Gly Asn Asn Val
340 345 350

Pro Ser Gly Asp Phe Ser Arg Glu Trp Ala Glu Ala Gln Arg Met Met
355 360 365

Arg Glu Leu Arg Asn Arg Asn Phe Gly Lys His Leu Arg Glu Ala Glu
370 375 380

Ala Asp Lys Arg Glu Ser Gln Leu Leu Leu Asn Arg Ile Arg Thr Trp
385 390 395 400

Gln Lys Thr His Gln Gly Glu Asn Asn Gly Leu Ala Asn Ser Ile Arg

405					410					415					
Asp	Ser	Leu	Asn	Glu	Tyr	Glu	Ala	Lys	Leu	Ser	Asp	Leu	Arg	Ala	Arg
			420					425					430		
Leu	Gln	Glu	Ala	Ala	Ala	Gln	Ala	Lys	Gln	Ala	Asn	Gly	Leu	Asn	Gln
		435					440					445			
Glu	Asn	Glu	Arg	Ala	Leu	Gly	Ala	Ile	Gln	Arg	Gln	Val	Lys	Glu	Ile
	450					455					460				
Asn	Ser	Leu	Gln	Ser	Asp	Phe	Thr	Lys	Tyr	Leu	Thr	Thr	Ala	Asp	Ser
465				470						475					480
Ser	Leu	Leu	Gln	Thr	Asn	Ile	Ala	Leu	Gln	Leu	Met	Glu	Lys	Ser	Gln
			485						490					495	
Lys	Glu	Tyr	Glu	Lys	Leu	Ala	Ala	Ser	Leu	Asn	Glu	Ala	Arg	Gln	Glu
			500					505					510		
Leu	Ser	Asp	Lys	Val	Arg	Glu	Leu	Ser	Arg	Ser	Ala	Gly	Lys	Thr	Ser
		515					520					525			
Leu	Val	Glu	Glu	Ala	Glu	Lys	His	Ala	Arg	Ser	Leu	Gln	Glu	Leu	Ala
	530					535					540				
Lys	Gln	Leu	Glu	Glu	Ile	Lys	Arg	Asn	Ala	Ser	Gly	Asp	Glu	Leu	Val
545					550				555						560
Arg	Cys	Ala	Val	Asp	Ala	Ala	Thr	Ala	Tyr	Glu	Asn	Ile	Leu	Asn	Ala
			565						570					575	
Ile	Lys	Ala	Ala	Glu	Asp	Ala	Ala	Asn	Arg	Ala	Ala	Ser	Ala	Ser	Glu
		580						585					590		
Ser	Ala	Leu	Gln	Thr	Val	Ile	Lys	Glu	Asp	Leu	Pro	Arg	Lys	Ala	Lys
		595					600					605			
Thr	Leu	Ser	Ser	Asn	Ser	Asp	Lys	Leu	Leu	Asn	Glu	Ala	Lys	Met	Thr
	610					615					620				
Gln	Lys	Lys	Leu	Lys	Gln	Glu	Val	Ser	Pro	Ala	Leu	Asn	Asn	Leu	Gln
625					630					635					640
Gln	Thr	Leu	Asn	Ile	Val	Thr	Val	Gln	Lys	Glu	Val	Ile	Asp	Thr	Asn
			645						650					655	
Leu	Thr	Thr	Leu	Arg	Asp	Gly	Leu	His	Gly	Ile	Gln	Arg	Gly	Asp	Ile
		660					665						670		
Asp	Ala	Met	Ile	Ser	Ser	Ala	Lys	Ser	Met	Val	Arg	Lys	Ala	Asn	Asp
		675					680					685			
Ile	Thr	Asp	Glu	Val	Leu	Asp	Gly	Leu	Asn	Pro	Ile	Gln	Thr	Asp	Val
	690					695					700				
Glu	Arg	Ile	Lys	Asp	Thr	Tyr	Gly	Arg	Thr	Gln	Asn	Glu	Asp	Phe	Lys
705					710					715					720
Lys	Ala	Leu	Thr	Asp	Ala	Asp	Asn	Ser	Val	Asn	Lys	Leu	Thr	Asn	Lys
			725						730					735	

Leu Pro Asp Leu Trp Arg Lys Ile Glu Ser Ile Asn Gln Gln Leu Leu
 740 745 750
 Pro Leu Gly Asn Ile Ser Asp Asn Met Asp Arg Ile Arg Glu Leu Ile
 755 760 765
 Gln Gln Ala Arg Asp Ala Ala Ser Lys Val Ala Val Pro Met Arg Phe
 770 775 780
 Asn Gly Lys Ser Gly Val Glu Val Arg Leu Pro Asn Asp Leu Glu Asp
 785 790 795 800
 Leu Lys Gly Tyr Thr Ser Leu Ser Leu Phe Leu Gln Arg Pro Asn Ser
 805 810 815
 Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr Leu Gly Asn
 820 825 830
 Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val Asp Gly Gln
 835 840 845
 Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu Leu Gln Val
 850 855 860
 Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val Met Asp Arg
 865 870 875 880
 Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn Tyr Thr Lys
 885 890 895
 Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr Asp Met Asp
 900 905 910
 Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu Asn Val Val
 915 920 925
 Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro Ser Arg Leu
 930 935 940
 Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp Leu Asn Glu
 945 950 955 960
 Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn Leu Asn Thr
 965 970 975
 Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser Asp Lys Asn
 980 985 990
 Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln Pro His Ala
 995 1000 1005
 Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val Asp Arg Gly
 1010 1015 1020
 Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Ile Ser Leu Asn Ile
 1025 1030 1035 1040
 Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser Glu Leu Pro
 1045 1050 1055

Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg Asp His Ser
1060 1065 1070

Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp Ile Asn Val
1075 1080 1085

Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp Phe Ser Thr
1090 1095 1100

Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg Phe Asn Ile
1105 1110 1115 1120

Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys Lys Thr Ser
1125 1130 1135

Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys Lys Cys Ser
1140 1145 1150

Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg Gly Gly Gln
1155 1160 1165

Leu Ser Phe Thr Asp Leu Gly Leu Pro Pro Thr Asp His Leu Gln Ala
1170 1175 1180

Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly Ile Leu Leu Asp His
1185 1190 1195 1200

Gln Thr Trp Thr Arg Asn Leu Gln Val Thr Leu Glu Asp Gly Tyr Ile
1205 1210 1215

Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile Phe Lys Ser Pro Gln
1220 1225 1230

Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser Val Ile Ser Asp Asn
1235 1240 1245

Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu Leu Arg Asn Ser Lys
1250 1255 1260

Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser Leu Arg Leu Gly Gly
1265 1270 1275 1280

Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe Val Gln Arg Leu Ser
1285 1290 1295

Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn Ser Leu Lys Arg Asp
1300 1305 1310

Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe Leu Met Leu
1315 1320 1325

Leu Lys Gly Ser Thr Arg Phe Asn Lys Thr Lys Thr Phe Arg Ile Asn
1330 1335 1340

Gln Leu Leu Gln Asp Thr Pro Val Ala Ser Pro Arg Ser Val Lys Val
1345 1350 1355 1360

Trp Gln Asp Ala Cys Ser Pro Leu Pro Lys Thr Gln Ala Asn His Gly
1365 1370 1375

Ala Leu Gln Phe Gly Asp Ile Pro Thr Ser His Leu Leu Phe Lys Leu

1380	1385	1390
Pro Gln Glu Leu Leu Lys	Pro Arg Ser Gln Phe	Ala Val Asp Met Gln
1395	1400	1405
Thr Thr Ser Ser Arg Gly	Leu Val Phe His Thr	Gly Thr Lys Asn Ser
1410	1415	1420
Phe Met Ala Leu Tyr Leu	Ser Lys Gly Arg Leu	Val Phe Ala Leu Gly
425	1430	1435 1440
Thr Asp Gly Lys Lys Leu	Arg Ile Lys Ser Lys	Glu Lys Cys Asn Asp
1445	1450	1455
Gly Lys Trp His Thr Val	Val Phe Gly His Asp	Gly Glu Lys Gly Arg
1460	1465	1470
Leu Val Val Asp Gly Leu	Arg Ala Arg Glu Gly	Ser Leu Pro Gly Asn
1475	1480	1485
Ser Thr Ile Ser Ile Arg	Ala Pro Val Tyr Leu	Gly Ser Pro Pro Ser
1490	1495	1500
Gly Lys Pro Lys Ser Leu	Pro Thr Asn Ser Phe	Val Gly Cys Leu Lys
505	1510	1515 1520
Asn Phe Gln Leu Asp Ser	Lys Pro Leu Tyr Thr	Pro Ser Ser Ser Phe
1525	1530	1535
Gly Val Ser Ser Cys Leu	Gly Gly Pro Leu Glu	Lys Gly Ile Tyr Phe
1540	1545	1550
Ser Glu Glu Gly Gly His	Val Val Leu Ala His	Ser Val Leu Leu Gly
1555	1560	1565
Pro Glu Phe Lys Leu Val	Phe Ser Ile Arg Pro	Arg Ser Leu Thr Gly
1570	1575	1580
Ile Leu Ile His Ile Gly	Ser Gln Pro Gly Lys	His Leu Cys Val Tyr
585	1590	1595 1600
Leu Glu Ala Gly Lys Val	Thr Ala Ser Met Asp	Ser Gly Ala Gly Gly
1605	1610	1615
Thr Ser Thr Ser Val Thr	Pro Lys Gln Ser Leu	Cys Asp Gly Gln Trp
1620	1625	1630
His Ser Val Ala Val Thr	Ile Lys Gln His Ile	Leu His Leu Glu Leu
1635	1640	1645
Asp Thr Asp Ser Ser Tyr	Thr Ala Gly Gln Ile	Pro Phe Pro Pro Ala
1650	1655	1660
Ser Thr Gln Glu Pro Leu	His Leu Gly Gly Ala	Pro Ala Asn Leu Thr
665	1670	1675 1680
Thr Leu Arg Ile Pro Val	Trp Lys Ser Phe Phe	Gly Cys Leu Arg Asn
1685	1690	1695
Ile His Val Asn His Ile	Pro Val Pro Val Thr	Glu Ala Leu Glu Val
1700	1705	1710

Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp Gln
 1715 1720

<210> 3
 <211> 5170
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(5079)

<400> 3
 cag caa agg gtg cca ttt ctt cag cct ccc ggt caa agt caa ctg caa 48
 Gln Gln Arg Val Pro Phe Leu Gln Pro Pro Gly Gln Ser Gln Leu Gln
 1 5 10 15
 gcg agt tat gtg gag ttt aga ccc agc cag ggt tgt agc cct gga tac 96
 Ala Ser Tyr Val Glu Phe Arg Pro Ser Gln Gly Cys Ser Pro Gly Tyr
 20 25 30
 tat cgg gat cat aaa ggc ttg tat acc gga cgg tgt gtt ccc tgc aat 144
 Tyr Arg Asp His Lys Gly Leu Tyr Thr Gly Arg Cys Val Pro Cys Asn
 35 40 45
 tgc aac gga cat tca aat caa tgc cag gat ggc tca ggc ata tgt gtt 192
 Cys Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser Gly Ile Cys Val
 50 55 60
 aac tgt cag cac aac acc gcg gga gag cac tgt gaa cgc tgc cag gag 240
 Asn Cys Gln His Asn Thr Ala Gly Glu His Cys Glu Arg Cys Gln Glu
 65 70 75 80
 ggc tac tat ggc aac gcc gtc cac gga tcc tgc agg gcc tgc cca tgt 288
 Gly Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg Ala Cys Pro Cys
 85 90 95
 cct cac act aac agc ttt gcc act ggc tgt gtg gtg aat ggg gga gac 336
 Pro His Thr Asn Ser Phe Ala Thr Gly Cys Val Val Asn Gly Gly Asp
 100 105 110
 gtg cgg tgc tcc tgc aaa gct ggg tac aca gga aca cag tgt gaa agg 384
 Val Arg Cys Ser Cys Lys Ala Gly Tyr Thr Gly Thr Gln Cys Glu Arg
 115 120 125
 tgt gca ccg gga tat ttc ggg aat ccc cag aaa ttc gga ggt agc tgc 432
 Cys Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe Gly Gly Ser Cys
 130 135 140
 caa cca tgc agt tgt aac agc aat ggc cag ctg ggc agc tgt cat ccc 480
 Gln Pro Cys Ser Cys Asn Ser Asn Gly Gln Leu Gly Ser Cys His Pro
 145 150 155 160
 ctg act gga gac tgc ata aac caa gaa ccc aaa gat agc agc cct gca 528
 Leu Thr Gly Asp Cys Ile Asn Gln Glu Pro Lys Asp Ser Ser Pro Ala
 165 170 175
 gaa gaa tgt gat gat tgc gac agc tgt gtg atg acc ctc ctg aac gac 576
 Glu Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr Leu Leu Asn Asp

180										185					190					
ctg gcc acc atg ggc gag cag ctc cgc ctg gtc aag tct cag ctg cag	624																			
Leu Ala Thr Met Gly Glu Gln Leu Arg Leu Val Lys Ser Gln Leu Gln																				
195 200 205																				
ggc ctg agt gcc agc gca ggg ctt ctg gag cag atg agg cac atg gag	672																			
Gly Leu Ser Ala Ser Ala Gly Leu Leu Glu Gln Met Arg His Met Glu																				
210 215 220																				
acc cag gcc aag gac ctg agg aat cag ttg ctc aac tac cgt tct gcc	720																			
Thr Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Asn Tyr Arg Ser Ala																				
225 230 235 240																				
att tca aat cat gga tca aaa ata gaa ggc ctg gaa aga gaa ctg act	768																			
Ile Ser Asn His Gly Ser Lys Ile Glu Gly Leu Glu Arg Glu Leu Thr																				
245 250 255																				
gat ttg aat caa gaa ttt gag act tta caa gaa aag gct caa gta aat	816																			
Asp Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys Ala Gln Val Asn																				
260 265 270																				
tcc aga aaa gca caa aca tta aac aac aat gtt aat cgg gca aca caa	864																			
Ser Arg Lys Ala Gln Thr Leu Asn Asn Asn Val Asn Arg Ala Thr Gln																				
275 280 285																				
agc gca aaa gaa cta gat gtg aag att aaa aat gtc atc cgg aat gtg	912																			
Ser Ala Lys Glu Leu Asp Val Lys Ile Lys Asn Val Ile Arg Asn Val																				
290 295 300																				
cac att ctt tta aag cag atc tct ggg aca gat gga gag gga aac aac	960																			
His Ile Leu Leu Lys Gln Ile Ser Gly Thr Asp Gly Glu Gly Asn Asn																				
305 310 315 320																				
gtg cct tca ggt gac ttt tcc aga gag tgg gct gaa gcc cag cgc atg	1008																			
Val Pro Ser Gly Asp Phe Ser Arg Glu Trp Ala Glu Ala Gln Arg Met																				
325 330 335																				
atg agg gaa ctg cgg aac agg aac ttt gga aag cac ctc aga gaa gca	1056																			
Met Arg Glu Leu Arg Asn Arg Asn Phe Gly Lys His Leu Arg Glu Ala																				
340 345 350																				
gaa gct gat aaa agg gag tcg cag ctc ttg ctg aac cgg ata agg acc	1104																			
Glu Ala Asp Lys Arg Glu Ser Gln Leu Leu Leu Asn Arg Ile Arg Thr																				
355 360 365																				
tgg cag aaa acc cac cag ggg gag aac aat ggg ctt gct aac agt atc	1152																			
Trp Gln Lys Thr His Gln Gly Glu Asn Asn Gly Leu Ala Asn Ser Ile																				
370 375 380																				
cgg gat tct tta aat gaa tac gaa gcc aaa ctc agt gac ctt cgt gct	1200																			
Arg Asp Ser Leu Asn Glu Tyr Glu Ala Lys Leu Ser Asp Leu Arg Ala																				
385 390 395 400																				
cgg ctg cag gag gca gct gcc caa gcc aag cag gca aat ggc ttg aac	1248																			
Arg Leu Gln Glu Ala Ala Ala Gln Ala Lys Gln Ala Asn Gly Leu Asn																				
405 410 415																				
caa gaa aac gag aga gct ttg gga gcc att cag aga caa gtg aaa gaa	1296																			
Gln Glu Asn Glu Arg Ala Leu Gly Ala Ile Gln Arg Gln Val Lys Glu																				
420 425 430																				

ata aat tcc ctg cag agt gat ttc acc aag tat cta acc act gca gac	1344
Ile Asn Ser Leu Gln Ser Asp Phe Thr Lys Tyr Leu Thr Thr Ala Asp	
435 440 445	
tca tct ttg ttg caa acc aac att gcg ctg cag ctg atg gag aaa agc	1392
Ser Ser Leu Leu Gln Thr Asn Ile Ala Leu Gln Leu Met Glu Lys Ser	
450 455 460	
cag aag gaa tat gaa aaa tta gct gcc agt tta aat gaa gca aga caa	1440
Gln Lys Glu Tyr Glu Lys Leu Ala Ala Ser Leu Asn Glu Ala Arg Gln	
465 470 475 480	
gaa cta agt gac aaa gta aga gaa ctt tcc aga tct gct ggc aaa aca	1488
Glu Leu Ser Asp Lys Val Arg Glu Leu Ser Arg Ser Ala Gly Lys Thr	
485 490 495	
tcc ctt gtg gag gag gca gaa aag cac gcg cgg tcc tta caa gag ctg	1536
Ser Leu Val Glu Glu Ala Glu Lys His Ala Arg Ser Leu Gln Glu Leu	
500 505 510	
gca aag cag ctg gaa gag atc aag aga aac gcc agc ggg gat gag ctg	1584
Ala Lys Gln Leu Glu Glu Ile Lys Arg Asn Ala Ser Gly Asp Glu Leu	
515 520 525	
gtg cgc tgt gct gtg gat gcc gcc acc gcc tac gag aac atc ctc aat	1632
Val Arg Cys Ala Val Asp Ala Ala Thr Ala Tyr Glu Asn Ile Leu Asn	
530 535 540	
gcc atc aaa gcg gcc gag gac gca gcc aac agg gct gcc agt gca tct	1680
Ala Ile Lys Ala Ala Glu Asp Ala Ala Asn Arg Ala Ala Ser Ala Ser	
545 550 555 560	
gaa tct gcc ctc cag aca gtg ata aag gaa gat ctg cca aga aaa gct	1728
Glu Ser Ala Leu Gln Thr Val Ile Lys Glu Asp Leu Pro Arg Lys Ala	
565 570 575	
aaa acc ctg agt tcc aac agt gat aaa ctg tta aat gaa gcc aag atg	1776
Lys Thr Leu Ser Ser Asn Ser Asp Lys Leu Leu Asn Glu Ala Lys Met	
580 585 590	
aca caa aag aag cta aag caa gaa gtc agt cca gct ctc aac aac cta	1824
Thr Gln Lys Lys Leu Lys Gln Glu Val Ser Pro Ala Leu Asn Asn Leu	
595 600 605	
cag caa acc ctg aat att gtg aca gtt cag aaa gaa gtg ata gac acc	1872
Gln Gln Thr Leu Asn Ile Val Thr Val Gln Lys Glu Val Ile Asp Thr	
610 615 620	
aat ctc aca act ctc cga gat ggt ctt cat ggg ata cag aga ggt gat	1920
Asn Leu Thr Thr Leu Arg Asp Gly Leu His Gly Ile Gln Arg Gly Asp	
625 630 635 640	
att gat gct atg atc agt agt gca aag agc atg gtc aga aag gcc aac	1968
Ile Asp Ala Met Ile Ser Ser Ala Lys Ser Met Val Arg Lys Ala Asn	
645 650 655	
gac atc aca gat gag gtt ctg gat ggg ctc aac ccc atc cag aca gat	2016
Asp Ile Thr Asp Glu Val Leu Asp Gly Leu Asn Pro Ile Gln Thr Asp	
660 665 670	

gtg gaa aga att aag gac acc tat ggg agg aca cag aac gaa gac ttc	2064
Val Glu Arg Ile Lys Asp Thr Tyr Gly Arg Thr Gln Asn Glu Asp Phe	
675 680 685	
aaa aag gct ctg act gat gca gat aac tcg gtg aat aag tta acc aac	2112
Lys Lys Ala Leu Thr Asp Ala Asp Asn Ser Val Asn Lys Leu Thr Asn	
690 695 700	
aaa cta cct gat ctt tgg cgc aag att gaa agt atc aac caa cag ctg	2160
Lys Leu Pro Asp Leu Trp Arg Lys Ile Glu Ser Ile Asn Gln Gln Leu	
705 710 715 720	
ttg ccc ttg gga aac atc tct gac aac atg gac aga ata cga gaa cta	2208
Leu Pro Leu Gly Asn Ile Ser Asp Asn Met Asp Arg Ile Arg Glu Leu	
725 730 735	
att cag cag gcc aga gat gct gcc agt aag gtt gct gtc ccc atg agg	2256
Ile Gln Gln Ala Arg Asp Ala Ala Ser Lys Val Ala Val Pro Met Arg	
740 745 750	
ttc aat ggt aaa tct gga gtc gaa gtc cga ctg cca aat gac ctg gaa	2304
Phe Asn Gly Lys Ser Gly Val Glu Val Arg Leu Pro Asn Asp Leu Glu	
755 760 765	
gat ttg aaa gga tat aca tct ctg tcc ttg ttt ctc caa agg ccc aac	2352
Asp Leu Lys Gly Tyr Thr Ser Leu Ser Leu Phe Leu Gln Arg Pro Asn	
770 775 780	
tca aga gaa aat ggg ggt act gag aat atg ttt gtg atg tac ctt gga	2400
Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr Leu Gly	
785 790 795 800	
aat aaa gat gcc tcc cgg gac tac atc ggc atg gca gtt gtg gat ggc	2448
Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val Asp Gly	
805 810 815	
cag ctc acc tgt gtc tac aac ctg ggg gac cgt gag gct gaa ctc caa	2496
Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu Leu Gln	
820 825 830	
gtg gac cag atc ttg acc aag agt gag act aag gag gca gtt atg gat	2544
Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val Met Asp	
835 840 845	
cgg gtg aaa ttt cag aga att tat cag ttt gca agg ctt aat tac acc	2592
Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn Tyr Thr	
850 855 860	
aaa gga gcc aca tcc agt aaa cca gaa aca ccc gga gtc tat gac atg	2640
Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr Asp Met	
865 870 875 880	
gat ggt aga aat agc aat aca ctc ctt aat ttg gat cct gaa aat gtt	2688
Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu Asn Val	
885 890 895	
gta ttt tat gtt gga ggt tac cca cct gat ttt aaa ctt ccc agt cga	2736
Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro Ser Arg	
900 905 910	
cta agt ttc cct cca tac aaa ggt tgt att gaa tta gat gac ctc aat	2784

Leu	Ser	Phe	Pro	Pro	Tyr	Lys	Gly	Cys	Ile	Glu	Leu	Asp	Asp	Leu	Asn	
		915					920					925				
gaa	aat	gtt	ctg	agc	ttg	tac	aac	ttc	aaa	aaa	aca	ttc	aat	ctc	aac	2832
Glu	Asn	Val	Leu	Ser	Leu	Tyr	Asn	Phe	Lys	Lys	Thr	Phe	Asn	Leu	Asn	
		930				935					940					
aca	act	gaa	gtg	gag	cct	tgt	aga	agg	agg	aag	gaa	gag	tca	gac	aaa	2880
Thr	Thr	Glu	Val	Glu	Pro	Cys	Arg	Arg	Arg	Lys	Glu	Glu	Ser	Asp	Lys	
945					950					955					960	
aat	tat	ttt	gaa	ggc	acg	ggc	tat	gct	cga	gtt	cca	act	caa	cca	cat	2928
Asn	Tyr	Phe	Glu	Gly	Thr	Gly	Tyr	Ala	Arg	Val	Pro	Thr	Gln	Pro	His	
				965				970						975		
gct	ccc	atc	cca	acc	ttt	gga	cag	aca	att	cag	acc	acc	gtg	gat	aga	2976
Ala	Pro	Ile	Pro	Thr	Phe	Gly	Gln	Thr	Ile	Gln	Thr	Thr	Val	Asp	Arg	
			980					985					990			
ggc	ttg	ctg	ttc	ttt	gca	gaa	aac	ggg	gat	cgc	ttc	ata	tct	cta	aat	3024
Gly	Leu	Leu	Phe	Phe	Ala	Glu	Asn	Gly	Asp	Arg	Phe	Ile	Ser	Leu	Asn	
		995					1000					1005				
ata	gaa	gat	ggc	aag	ctc	atg	gtg	aga	tac	aaa	ctg	aat	tca	gag	cta	3072
Ile	Glu	Asp	Gly	Lys	Leu	Met	Val	Arg	Tyr	Lys	Leu	Asn	Ser	Glu	Leu	
		1010				1015					1020					
cca	aaa	gag	aga	gga	gtt	gga	gac	gcc	ata	aac	aac	ggc	aga	gac	cat	3120
Pro	Lys	Glu	Arg	Gly	Val	Gly	Asp	Ala	Ile	Asn	Asn	Gly	Arg	Asp	His	
1025					1030					1035					1040	
tcg	att	cag	atc	aaa	att	gga	aaa	ctc	caa	aag	cgt	atg	tgg	ata	aat	3168
Ser	Ile	Gln	Ile	Lys	Ile	Gly	Lys	Leu	Gln	Lys	Arg	Met	Trp	Ile	Asn	
				1045					1050					1055		
gtg	gac	gtt	caa	aac	act	ata	att	gat	ggc	gaa	gta	ttt	gat	ttc	agc	3216
Val	Asp	Val	Gln	Asn	Thr	Ile	Ile	Asp	Gly	Glu	Val	Phe	Asp	Phe	Ser	
			1060					1065					1070			
aca	tat	tat	ctg	gga	gga	att	cca	att	gca	atc	agg	gaa	aga	ttt	aac	3264
Thr	Tyr	Tyr	Leu	Gly	Gly	Ile	Pro	Ile	Ala	Ile	Arg	Glu	Arg	Phe	Asn	
		1075					1080				1085					
att	tct	acg	cct	gct	ttc	cga	ggc	tgc	atg	aaa	aat	ttg	aag	aaa	acc	3312
Ile	Ser	Thr	Pro	Ala	Phe	Arg	Gly	Cys	Met	Lys	Asn	Leu	Lys	Lys	Thr	
		1090				1095					1100					
agt	ggc	gtc	gtt	aga	ttg	aat	gat	act	gtg	gga	gta	acc	aaa	aag	tgc	3360
Ser	Gly	Val	Val	Arg	Leu	Asn	Asp	Thr	Val	Gly	Val	Thr	Lys	Lys	Cys	
1105					1110					1115					1120	
tcg	gaa	gac	tgg	aag	ctt	gtg	cga	tct	gcc	tca	ttc	tcc	aga	gga	gga	3408
Ser	Glu	Asp	Trp	Lys	Leu	Val	Arg	Ser	Ala	Ser	Phe	Ser	Arg	Gly	Gly	
			1125						1130					1135		
caa	ttg	agt	ttc	act	gat	ttg	ggc	tta	cca	cct	act	gac	cac	ctc	cag	3456
Gln	Leu	Ser	Phe	Thr	Asp	Leu	Gly	Leu	Pro	Pro	Thr	Asp	His	Leu	Gln	
			1140					1145					1150			
gcc	tca	ttt	gga	ttt	cag	acc	ttt	caa	ccc	agt	ggc	ata	tta	tta	gat	3504
Ala	Ser	Phe	Gly	Phe	Gln	Thr	Phe	Gln	Pro	Ser	Gly	Ile	Leu	Leu	Asp	

1155	1160	1165	
cat cag aca tgg aca agg aac ctg cag gtc act ctg gaa gat ggt tac			3552
His Gln Thr Trp Thr Arg Asn Leu Gln Val Thr Leu Glu Asp Gly Tyr			
1170	1175	1180	
att gaa ttg agc acc agc gat agc ggc ggc cca att ttt aaa tct cca			3600
Ile Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile Phe Lys Ser Pro			
1185	1190	1195	1200
cag acg tat atg gat ggt tta ctg cat tat gta tct gta ata agc gac			3648
Gln Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser Val Ile Ser Asp			
1205	1210	1215	
aac tct gga cta cgg ctt ctc atc gat gac cag ctt ctg aga aat agc			3696
Asn Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu Leu Arg Asn Ser			
1220	1225	1230	
aaa agg cta aaa cac att tca agt tcc cgg cag tct ctg cgt ctg ggc			3744
Lys Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser Leu Arg Leu Gly			
1235	1240	1245	
ggg agc aat ttt gag ggt tgt att agc aat gtt ttt gtc cag agg tta			3792
Gly Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe Val Gln Arg Leu			
1250	1255	1260	
tca ctg agt cct gaa gtc cta gat ttg acc agt aac tct ctc aag aga			3840
Ser Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn Ser Leu Lys Arg			
1265	1270	1275	1280
gat gtg tcc ctg gga ggc tgc agt tta aac aaa cca cct ttt cta atg			3888
Asp Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe Leu Met			
1285	1290	1295	
ttg ctt aaa ggt tct acc agg ttt aac aag acc aag act ttt cgt atc			3936
Leu Leu Lys Gly Ser Thr Arg Phe Asn Lys Thr Lys Thr Phe Arg Ile			
1300	1305	1310	
aac cag ctg ttg cag gac aca cca gtg gcc tcc cca agg agc gtg aag			3984
Asn Gln Leu Leu Gln Asp Thr Pro Val Ala Ser Pro Arg Ser Val Lys			
1315	1320	1325	
gtg tgg caa gat gct tgc tca cca ctt ccc aag acc cag gcc aat cat			4032
Val Trp Gln Asp Ala Cys Ser Pro Leu Pro Lys Thr Gln Ala Asn His			
1330	1335	1340	
gga gcc ctc cag ttt ggg gac att ccc acc agc cac ttg cta ttc aag			4080
Gly Ala Leu Gln Phe Gly Asp Ile Pro Thr Ser His Leu Leu Phe Lys			
1345	1350	1355	1360
ctt cct cag gag ctg ctg aaa ccc agg tca cag ttt gct gtg gac atg			4128
Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser Gln Phe Ala Val Asp Met			
1365	1370	1375	
cag aca aca tcc tcc aga gga ctg gtg ttt cac acg ggc act aag aac			4176
Gln Thr Thr Ser Ser Arg Gly Leu Val Phe His Thr Gly Thr Lys Asn			
1380	1385	1390	
tcc ttt atg gct ctt tat ctt tca aaa gga cgt ctg gtc ttt gca ctg			4224
Ser Phe Met Ala Leu Tyr Leu Ser Lys Gly Arg Leu Val Phe Ala Leu			
1395	1400	1405	

ggg aca gat ggg aaa aaa ttg agg atc aaa agc aag gag aaa tgc aat	4272
Gly Thr Asp Gly Lys Lys Leu Arg Ile Lys Ser Lys Glu Lys Cys Asn	
1410 1415 1420	
gat ggg aaa tgg cac acg gtg gtg ttt ggc cat gat ggg gaa aag ggg	4320
Asp Gly Lys Trp His Thr Val Val Phe Gly His Asp Gly Glu Lys Gly	
1425 1430 1435 1440	
cgc ttg gtt gtg gat gga ctg agg gcc cgg gag gga agt ttg cct gga	4368
Arg Leu Val Val Asp Gly Leu Arg Ala Arg Glu Gly Ser Leu Pro Gly	
1445 1450 1455	
aac tcc acc atc agc atc aga gcg cca gtt tac ctg gga tca cct cca	4416
Asn Ser Thr Ile Ser Ile Arg Ala Pro Val Tyr Leu Gly Ser Pro Pro	
1460 1465 1470	
tca ggg aaa cca aag agc ctc ccc aca aac agc ttt gtg gga tgc ctg	4464
Ser Gly Lys Pro Lys Ser Leu Pro Thr Asn Ser Phe Val Gly Cys Leu	
1475 1480 1485	
aag aac ttt cag ctg gat tca aaa ccc ttg tat acc cct tct tca agc	4512
Lys Asn Phe Gln Leu Asp Ser Lys Pro Leu Tyr Thr Pro Ser Ser Ser	
1490 1495 1500	
ttc ggg gtg tct tcc tgc ttg ggt ggt cct ttg gag aaa ggc att tat	4560
Phe Gly Val Ser Ser Cys Leu Gly Gly Pro Leu Glu Lys Gly Ile Tyr	
1505 1510 1515 1520	
ttc tct gaa gaa gga ggt cat gtc gtc ttg gct cac tct gta ttg ttg	4608
Phe Ser Glu Glu Gly Gly His Val Val Leu Ala His Ser Val Leu Leu	
1525 1530 1535	
ggg cca gaa ttt aag ctt gtt ttc agc atc cgc cca aga agt ctc act	4656
Gly Pro Glu Phe Lys Leu Val Phe Ser Ile Arg Pro Arg Ser Leu Thr	
1540 1545 1550	
ggg atc cta ata cac atc gga agt cag ccc ggg aag cac tta tgt gtt	4704
Gly Ile Leu Ile His Ile Gly Ser Gln Pro Gly Lys His Leu Cys Val	
1555 1560 1565	
tac ctg gag gca gga aag gtc acg gcc tct atg gac agt ggg gca ggt	4752
Tyr Leu Glu Ala Gly Lys Val Thr Ala Ser Met Asp Ser Gly Ala Gly	
1570 1575 1580	
ggg acc tca acg tcg gtc aca cca aag cag tct ctg tgt gat gga cag	4800
Gly Thr Ser Thr Ser Val Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln	
1585 1590 1595 1600	
tgg cac tcg gtg gca gtc acc ata aaa caa cac atc ctg cac ctg gaa	4848
Trp His Ser Val Ala Val Thr Ile Lys Gln His Ile Leu His Leu Glu	
1605 1610 1615	
ctg gac aca gac agt agc tac aca gct gga cag atc ccc ttc cca cct	4896
Leu Asp Thr Asp Ser Ser Tyr Thr Ala Gly Gln Ile Pro Phe Pro Pro	
1620 1625 1630	
gcc agc act caa gag cca cta cac ctt gga ggt gct cca gcc aat ttg	4944
Ala Ser Thr Gln Glu Pro Leu His Leu Gly Gly Ala Pro Ala Asn Leu	
1635 1640 1645	

acg aca ctg agg atc cct gtg tgg aaa tca ttc ttt ggc tgt ctg agg 4992
 Thr Thr Leu Arg Ile Pro Val Trp Lys Ser Phe Phe Gly Cys Leu Arg
 1650 1655 1660

aat att cat gtc aat cac atc cct gtc cct gtc act gaa gcc ttg gaa 5040
 Asn Ile His Val Asn His Ile Pro Val Pro Val Thr Glu Ala Leu Glu
 1665 1670 1675 1680

gtc cag ggg cct gtc agt ctg aat ggt tgt cct gac cag taacccaagc 5089
 Val Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp Gln
 1685 1690

ctatttcaca gcaaggaaat tcaccttcaa aagcactgat tacccaatgc acctccctcc 5149

ccagctcgag atcattcttc a 5170

<210> 4
 <211> 1693
 <212> PRT
 <213> Homo sapiens

<400> 4
 Gln Gln Arg Val Pro Phe Leu Gln Pro Pro Gly Gln Ser Gln Leu Gln
 1 5 10 15

Ala Ser Tyr Val Glu Phe Arg Pro Ser Gln Gly Cys Ser Pro Gly Tyr
 20 25 30

Tyr Arg Asp His Lys Gly Leu Tyr Thr Gly Arg Cys Val Pro Cys Asn
 35 40 45

Cys Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser Gly Ile Cys Val
 50 55 60

Asn Cys Gln His Asn Thr Ala Gly Glu His Cys Glu Arg Cys Gln Glu
 65 70 75 80

Gly Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg Ala Cys Pro Cys
 85 90 95

Pro His Thr Asn Ser Phe Ala Thr Gly Cys Val Val Asn Gly Gly Asp
 100 105 110

Val Arg Cys Ser Cys Lys Ala Gly Tyr Thr Gly Thr Gln Cys Glu Arg
 115 120 125

Cys Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe Gly Gly Ser Cys
 130 135 140

Gln Pro Cys Ser Cys Asn Ser Asn Gly Gln Leu Gly Ser Cys His Pro
 145 150 155 160

Leu Thr Gly Asp Cys Ile Asn Gln Glu Pro Lys Asp Ser Ser Pro Ala
 165 170 175

Glu Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr Leu Leu Asn Asp
 180 185 190

Leu Ala Thr Met Gly Glu Gln Leu Arg Leu Val Lys Ser Gln Leu Gln
 195 200 205

Gly Leu Ser Ala Ser Ala Gly Leu Leu Glu Gln Met Arg His Met Glu
210 215 220

Thr Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Asn Tyr Arg Ser Ala
225 230 235 240

Ile Ser Asn His Gly Ser Lys Ile Glu Gly Leu Glu Arg Glu Leu Thr
245 250 255

Asp Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys Ala Gln Val Asn
260 265 270

Ser Arg Lys Ala Gln Thr Leu Asn Asn Asn Val Asn Arg Ala Thr Gln
275 280 285

Ser Ala Lys Glu Leu Asp Val Lys Ile Lys Asn Val Ile Arg Asn Val
290 295 300

His Ile Leu Leu Lys Gln Ile Ser Gly Thr Asp Gly Glu Gly Asn Asn
305 310 315 320

Val Pro Ser Gly Asp Phe Ser Arg Glu Trp Ala Glu Ala Gln Arg Met
325 330 335

Met Arg Glu Leu Arg Asn Arg Asn Phe Gly Lys His Leu Arg Glu Ala
340 345 350

Glu Ala Asp Lys Arg Glu Ser Gln Leu Leu Leu Asn Arg Ile Arg Thr
355 360 365

Trp Gln Lys Thr His Gln Gly Glu Asn Asn Gly Leu Ala Asn Ser Ile
370 375 380

Arg Asp Ser Leu Asn Glu Tyr Glu Ala Lys Leu Ser Asp Leu Arg Ala
385 390 395 400

Arg Leu Gln Glu Ala Ala Ala Gln Ala Lys Gln Ala Asn Gly Leu Asn
405 410 415

Gln Glu Asn Glu Arg Ala Leu Gly Ala Ile Gln Arg Gln Val Lys Glu
420 425 430

Ile Asn Ser Leu Gln Ser Asp Phe Thr Lys Tyr Leu Thr Thr Ala Asp
435 440 445

Ser Ser Leu Leu Gln Thr Asn Ile Ala Leu Gln Leu Met Glu Lys Ser
450 455 460

Gln Lys Glu Tyr Glu Lys Leu Ala Ala Ser Leu Asn Glu Ala Arg Gln
465 470 475 480

Glu Leu Ser Asp Lys Val Arg Glu Leu Ser Arg Ser Ala Gly Lys Thr
485 490 495

Ser Leu Val Glu Glu Ala Glu Lys His Ala Arg Ser Leu Gln Glu Leu
500 505 510

Ala Lys Gln L u Glu Glu Ile Lys Arg Asn Ala S r Gly Asp Glu Leu
515 520 525

Val Arg Cys Ala Val Asp Ala Ala Thr Ala Tyr Glu Asn Ile Leu Asn
530 535 540

Ala Ile Lys Ala Ala Glu Asp Ala Ala Asn Arg Ala Ala Ser Ala Ser
545 550 555 560

Glu Ser Ala Leu Gln Thr Val Ile Lys Glu Asp Leu Pro Arg Lys Ala
565 570 575

Lys Thr Leu Ser Ser Asn Ser Asp Lys Leu Leu Asn Glu Ala Lys Met
580 585 590

Thr Gln Lys Lys Leu Lys Gln Glu Val Ser Pro Ala Leu Asn Asn Leu
595 600 605

Gln Gln Thr Leu Asn Ile Val Thr Val Gln Lys Glu Val Ile Asp Thr
610 615 620

Asn Leu Thr Thr Leu Arg Asp Gly Leu His Gly Ile Gln Arg Gly Asp
625 630 635 640

Ile Asp Ala Met Ile Ser Ser Ala Lys Ser Met Val Arg Lys Ala Asn
645 650 655

Asp Ile Thr Asp Glu Val Leu Asp Gly Leu Asn Pro Ile Gln Thr Asp
660 665 670

Val Glu Arg Ile Lys Asp Thr Tyr Gly Arg Thr Gln Asn Glu Asp Phe
675 680 685

Lys Lys Ala Leu Thr Asp Ala Asp Asn Ser Val Asn Lys Leu Thr Asn
690 695 700

Lys Leu Pro Asp Leu Trp Arg Lys Ile Glu Ser Ile Asn Gln Gln Leu
705 710 715 720

Leu Pro Leu Gly Asn Ile Ser Asp Asn Met Asp Arg Ile Arg Glu Leu
725 730 735

Ile Gln Gln Ala Arg Asp Ala Ala Ser Lys Val Ala Val Pro Met Arg
740 745 750

Phe Asn Gly Lys Ser Gly Val Glu Val Arg Leu Pro Asn Asp Leu Glu
755 760 765

Asp Leu Lys Gly Tyr Thr Ser Leu Ser Leu Phe Leu Gln Arg Pro Asn
770 775 780

Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr Leu Gly
785 790 795 800

Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val Asp Gly
805 810 815

Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu Leu Gln
820 825 830

Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val Met Asp
835 840 845

Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn Tyr Thr

850	855	860
Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr Asp Met 865 870 875 880		
Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu Asn Val 885 890 895		
Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro Ser Arg 900 905 910		
Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp Leu Asn 915 920 925		
Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn Leu Asn 930 935 940		
Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser Asp Lys 945 950 955 960		
Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln Pro His 965 970 975		
Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val Asp Arg 980 985 990		
Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Ile Ser Leu Asn 995 1000 1005		
Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser Glu Leu 1010 1015 1020		
Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg Asp His 1025 1030 1035 1040		
Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp Ile Asn 1045 1050 1055		
Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp Phe Ser 1060 1065 1070		
Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg Phe Asn 1075 1080 1085		
Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys Lys Thr 1090 1095 1100		
Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys Lys Cys 1105 1110 1115 1120		
Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg Gly Gly 1125 1130 1135		
Gln Leu Ser Phe Thr Asp Leu Gly Leu Pro Pro Thr Asp His Leu Gln 1140 1145 1150		
Ala Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly Ile Leu Leu Asp 1155 1160 1165		
His Gln Thr Trp Thr Arg Asn Leu Gln Val Thr Leu Glu Asp Gly Tyr 1170 1175 1180		

Ile Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile Phe Lys Ser Pro
1185 1190 1195 1200

Gln Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser Val Ile Ser Asp
1205 1210 1215

Asn Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu Leu Arg Asn Ser
1220 1225 1230

Lys Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser Leu Arg Leu Gly
1235 1240 1245

Gly Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe Val Gln Arg Leu
1250 1255 1260

Ser Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn Ser Leu Lys Arg
1265 1270 1275 1280

Asp Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe Leu Met
1285 1290 1295

Leu Leu Lys Gly Ser Thr Arg Phe Asn Lys Thr Lys Thr Phe Arg Ile
1300 1305 1310

Asn Gln Leu Leu Gln Asp Thr Pro Val Ala Ser Pro Arg Ser Val Lys
1315 1320 1325

Val Trp Gln Asp Ala Cys Ser Pro Leu Pro Lys Thr Gln Ala Asn His
1330 1335 1340

Gly Ala Leu Gln Phe Gly Asp Ile Pro Thr Ser His Leu Leu Phe Lys
1345 1350 1355 1360

Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser Gln Phe Ala Val Asp Met
1365 1370 1375

Gln Thr Thr Ser Ser Arg Gly Leu Val Phe His Thr Gly Thr Lys Asn
1380 1385 1390

Ser Phe Met Ala Leu Tyr Leu Ser Lys Gly Arg Leu Val Phe Ala Leu
1395 1400 1405

Gly Thr Asp Gly Lys Lys Leu Arg Ile Lys Ser Lys Glu Lys Cys Asn
1410 1415 1420

Asp Gly Lys Trp His Thr Val Val Phe Gly His Asp Gly Glu Lys Gly
1425 1430 1435 1440

Arg Leu Val Val Asp Gly Leu Arg Ala Arg Glu Gly Ser Leu Pro Gly
1445 1450 1455

Asn Ser Thr Ile Ser Ile Arg Ala Pro Val Tyr Leu Gly Ser Pro Pro
1460 1465 1470

Ser Gly Lys Pro Lys Ser Leu Pro Thr Asn Ser Phe Val Gly Cys Leu
1475 1480 1485

Lys Asn Phe Gln L u Asp Ser Lys Pro Leu Tyr Thr Pro Ser Ser Ser
1490 1495 1500

Phe Gly Val Ser Ser Cys Leu Gly Gly Pro Leu Glu Lys Gly Ile Tyr
 1505 1510 1515 1520

Phe Ser Glu Glu Gly Gly His Val Val Leu Ala His Ser Val Leu Leu
 1525 1530 1535

Gly Pro Glu Phe Lys Leu Val Phe Ser Ile Arg Pro Arg Ser Leu Thr
 1540 1545 1550

Gly Ile Leu Ile His Ile Gly Ser Gln Pro Gly Lys His Leu Cys Val
 1555 1560 1565

Tyr Leu Glu Ala Gly Lys Val Thr Ala Ser Met Asp Ser Gly Ala Gly
 1570 1575 1580

Gly Thr Ser Thr Ser Val Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln
 1585 1590 1595 1600

Trp His Ser Val Ala Val Thr Ile Lys Gln His Ile Leu His Leu Glu
 1605 1610 1615

Leu Asp Thr Asp Ser Ser Tyr Thr Ala Gly Gln Ile Pro Phe Pro Pro
 1620 1625 1630

Ala Ser Thr Gln Glu Pro Leu His Leu Gly Gly Ala Pro Ala Asn Leu
 1635 1640 1645

Thr Thr Leu Arg Ile Pro Val Trp Lys Ser Phe Phe Gly Cys Leu Arg
 1650 1655 1660

Asn Ile His Val Asn His Ile Pro Val Pro Val Thr Glu Ala Leu Glu
 1665 1670 1675 1680

Val Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp Gln
 1685 1690

<210> 5

<211> 5433

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (5139)

<220>

<221> sig_peptide

<222> (1) .. (60)

<400> 5

atg gga tgg ctg tgg atc ttt ggg gca gcc ctg ggg cag tgt ctg ggc 48
 Met Gly Trp Leu Trp Ile Phe Gly Ala Ala Leu Gly Gln Cys Leu Gly
 1 5 10 15

tac agt tca cag cag caa agg gtg cca ttt ctt cag cct ccc ggt caa 96
 Tyr Ser Ser Gln Gln Gln Arg Val Pro Phe Leu Gln Pro Pro Gly Gln
 20 25 30

agt caa ctg caa gcg agt tat gtg gag ttt aga ccc agc cag ggt tgt 144
 Ser Gln Leu Gln Ala Ser Tyr Val Glu Phe Arg Pro Ser Gln Gly Cys

35	40	45	
agc cct gga tac tat cgg gat cat aaa ggc ttg tat acc gga cgg tgt			192
Ser Pro Gly Tyr Tyr Arg Asp His Lys Gly Leu Tyr Thr Gly Arg Cys			
50	55	60	
ggt ccc tgc aat tgc aac gga cat tca aat caa tgc cag gat ggc tca			240
Val Pro Cys Asn Cys Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser			
65	70	75	80
ggc ata tgt gtt aac tgt cag cac aac acc gcg gga gag cac tgt gaa			288
Gly Ile Cys Val Asn Cys Gln His Asn Thr Ala Gly Glu His Cys Glu			
85	90	95	
cgc tgc cag gag ggc tac tat ggc aac gcc gtc cac gga tcc tgc agg			336
Arg Cys Gln Glu Gly Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg			
100	105	110	
gcc tgc cca tgt cct cac act aac agc ttt gcc act ggc tgt gtg gtg			384
Ala Cys Pro Cys Pro His Thr Asn Ser Phe Ala Thr Gly Cys Val Val			
115	120	125	
aat ggg gga gac gtg cgg tgc tcc tgc aaa gct ggg tac aca gga aca			432
Asn Gly Gly Asp Val Arg Cys Ser Cys Lys Ala Gly Tyr Thr Gly Thr			
130	135	140	
cag tgt gaa agg tgt gca ccg gga tat ttc ggg aat ccc cag aaa ttc			480
Gln Cys Glu Arg Cys Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe			
145	150	155	160
gga ggt agc tgc caa cca tgc agt tgt aac agc aat ggc cag ctg ggc			528
Gly Gly Ser Cys Gln Pro Cys Ser Cys Asn Ser Asn Gly Gln Leu Gly			
165	170	175	
agc tgt cat ccc ctg act gga gac tgc ata aac caa gaa ccc aaa gat			576
Ser Cys His Pro Leu Thr Gly Asp Cys Ile Asn Gln Glu Pro Lys Asp			
180	185	190	
agc agc cct gca gaa gaa tgt gat gat tgc gac agc tgt gtg atg acc			624
Ser Ser Pro Ala Glu Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr			
195	200	205	
ctc ctg aac gac ctg gcc acc atg ggc gag cag ctc cgc ctg gtc aag			672
Leu Leu Asn Asp Leu Ala Thr Met Gly Glu Gln Leu Arg Leu Val Lys			
210	215	220	
tct cag ctg cag ggc ctg agt gcc agc gca ggg ctt ctg gag cag atg			720
Ser Gln Leu Gln Gly Leu Ser Ala Ser Ala Gly Leu Leu Glu Gln Met			
225	230	235	240
agg cac atg gag acc cag gcc aag gac ctg agg aat cag ttg ctc aac			768
Arg His Met Glu Thr Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Asn			
245	250	255	
tac cgt tct gcc att tca aat cat gga tca aaa ata gaa ggc ctg gaa			816
Tyr Arg Ser Ala Ile Ser Asn His Gly Ser Lys Ile Glu Gly Leu Glu			
260	265	270	
aga gaa ctg act gat ttg aat caa gaa ttt gag act ttg caa gaa aag			864
Arg Glu Leu Thr Asp Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys			
275	280	285	

gct caa gta aat tcc aga aaa gca caa aca tta aac aac aat gtt aat	912
Ala Gln Val Asn Ser Arg Lys Ala Gln Thr Leu Asn Asn Asn Val Asn	
290 295 300	
cgg gca aca caa agc gca aaa gaa ctg gat gtg aag att aaa aat gtc	960
Arg Ala Thr Gln Ser Ala Lys Glu Leu Asp Val Lys Ile Lys Asn Val	
305 310 315 320	
atc cgg aat gtg cac att ctt tta aag cag atc tct ggg aca gat gga	1008
Ile Arg Asn Val His Ile Leu Leu Lys Gln Ile Ser Gly Thr Asp Gly	
325 330 335	
gag gga aac aac gtg cct tca ggt gac ttt tcc aga gag tgg gct gaa	1056
Glu Gly Asn Asn Val Pro Ser Gly Asp Phe Ser Arg Glu Trp Ala Glu	
340 345 350	
gcc cag cgc atg atg agg gaa ctg cgg aac agg aac ttt gga aag cac	1104
Ala Gln Arg Met Met Arg Glu Leu Arg Asn Arg Asn Phe Gly Lys His	
355 360 365	
ctc aga gaa gca gaa gct gat aaa agg gag tcg cag ctc ttg ctg aac	1152
Leu Arg Glu Ala Glu Ala Asp Lys Arg Glu Ser Gln Leu Leu Leu Asn	
370 375 380	
cgg ata agg acc tgg cag aaa acc cac cag ggg gag aac aat ggg ctt	1200
Arg Ile Arg Thr Trp Gln Lys Thr His Gln Gly Glu Asn Asn Gly Leu	
385 390 395 400	
gct aac agt atc cgg gat tct tta aat gaa tac gaa gcc aaa ctc agt	1248
Ala Asn Ser Ile Arg Asp Ser Leu Asn Glu Tyr Glu Ala Lys Leu Ser	
405 410 415	
gac ctt cgt gct cgg ctg cag gag gca gct gcc caa gcc aag cag gca	1296
Asp Leu Arg Ala Arg Leu Gln Glu Ala Ala Ala Gln Ala Lys Gln Ala	
420 425 430	
aat ggc ttg aac caa gaa aac gag aga gct ttg gga gcc att cag aga	1344
Asn Gly Leu Asn Gln Glu Asn Glu Arg Ala Leu Gly Ala Ile Gln Arg	
435 440 445	
caa gtg aaa gaa ata aat tcc ctg cag agt gat ttc acc aag tat cta	1392
Gln Val Lys Glu Ile Asn Ser Leu Gln Ser Asp Phe Thr Lys Tyr Leu	
450 455 460	
acc act gca gac tca tct ttg ttg caa acc aac att gcg ctg cag ctg	1440
Thr Thr Ala Asp Ser Ser Leu Leu Gln Thr Asn Ile Ala Leu Gln Leu	
465 470 475 480	
atg gag aaa agc cag aag gaa tat gaa aaa tta gct gcc agt tta aat	1488
Met Glu Lys Ser Gln Lys Glu Tyr Glu Lys Leu Ala Ala Ser Leu Asn	
485 490 495	
gaa gca aga caa gaa cta agt gac aaa gta aga gaa ctt tcc aga tct	1536
Glu Ala Arg Gln Glu Leu Ser Asp Lys Val Arg Glu Leu Ser Arg Ser	
500 505 510	
gct ggc aaa aca tcc ctt gtg gag gag gca gaa aag cac gcg cgg tcc	1584
Ala Gly Lys Thr Ser Leu Val Glu Glu Ala Glu Lys His Ala Arg Ser	
515 520 525	

tta caa gag ctg gca aag cag ctg gaa gag atc aag aga aac gcc agc	1632
Leu Gln Glu Leu Ala Lys Gln Leu Glu Glu Ile Lys Arg Asn Ala Ser	
530 535 540	
ggg gat gag ctg gtg cgc tgt gct gtg gat gcc gcc acc gcc tac gag	1680
Gly Asp Glu Leu Val Arg Cys Ala Val Asp Ala Ala Thr Ala Tyr Glu	
545 550 555 560	
aac atc ctc aat gcc atc aaa gcg gcc gag gac gca gcc aac agg gct	1728
Asn Ile Leu Asn Ala Ile Lys Ala Ala Glu Asp Ala Ala Asn Arg Ala	
565 570 575	
gcc agt gca tct gaa tct gcc ctc cag aca gtg ata aag gaa gat ctg	1776
Ala Ser Ala Ser Glu Ser Ala Leu Gln Thr Val Ile Lys Glu Asp Leu	
580 585 590	
cca aga aaa gct aaa acc ctg agt tcc aac agt gat aaa ctg tta aat	1824
Pro Arg Lys Ala Lys Thr Leu Ser Ser Asn Ser Asp Lys Leu Leu Asn	
595 600 605	
gaa gcc aag atg aca caa aag aag cta aag caa gaa gtc agt cca gct	1872
Glu Ala Lys Met Thr Gln Lys Lys Leu Lys Gln Glu Val Ser Pro Ala	
610 615 620	
ctc aac aac cta cag caa acc ctg aat att gtg aca gtt cag aaa gaa	1920
Leu Asn Asn Leu Gln Gln Thr Leu Asn Ile Val Thr Val Gln Lys Glu	
625 630 635 640	
gtg ata gac acc aat ctc aca act ctc cga gat ggt ctt cat ggg ata	1968
Val Ile Asp Thr Asn Leu Thr Thr Leu Arg Asp Gly Leu His Gly Ile	
645 650 655	
cag aga ggt gat att gat gct atg atc agt agt gca aag agc atg gtc	2016
Gln Arg Gly Asp Ile Asp Ala Met Ile Ser Ser Ala Lys Ser Met Val	
660 665 670	
aga aag gcc aac gac atc aca gat gag gtt ctg gat ggg ctc aac ccc	2064
Arg Lys Ala Asn Asp Ile Thr Asp Glu Val Leu Asp Gly Leu Asn Pro	
675 680 685	
atc cag aca gat gtg gaa aga att aag gac acc tat ggg agg aca cag	2112
Ile Gln Thr Asp Val Glu Arg Ile Lys Asp Thr Tyr Gly Arg Thr Gln	
690 695 700	
aac gaa gac ttc aaa aag gct ctg act gat gca gat aac tcg gtg aat	2160
Asn Glu Asp Phe Lys Lys Ala Leu Thr Asp Ala Asp Asn Ser Val Asn	
705 710 715 720	
aag tta acc aac aaa cta cct gat ctt tgg cgc aag att gaa agt atc	2208
Lys Leu Thr Asn Lys Leu Pro Asp Leu Trp Arg Lys Ile Glu Ser Ile	
725 730 735	
aac caa cag ctg ttg ccc ttg gga aac atc tct gac aac atg gac aga	2256
Asn Gln Gln Leu Leu Pro Leu Gly Asn Ile Ser Asp Asn Met Asp Arg	
740 745 750	
ata cga gaa cta att cag cag gcc aga gat gct gcc agt aag gtt gct	2304
Ile Arg Glu Leu Ile Gln Gln Ala Arg Asp Ala Ala Ser Lys Val Ala	
755 760 765	
gtc ccc atg agg ttc aat ggt aaa tct gga gtc gaa gtc cga ctg cca	2352

Val	Pro	Met	Arg	Phe	Asn	Gly	Lys	Ser	Gly	Val	Glu	Val	Arg	Leu	Pro		
770						775					780						
aat	gac	ctg	gaa	gat	ttg	aaa	gga	tat	aca	tct	ctg	tcc	ttg	ttt	ctc	2400	
Asn	Asp	Leu	Glu	Asp	Leu	Lys	Gly	Tyr	Thr	Ser	Leu	Ser	Leu	Phe	Leu		
785					790					795					800		
caa	agg	ccc	aac	tca	aga	gaa	aat	ggg	ggt	act	gag	aat	atg	ttt	gtg	2448	
Gln	Arg	Pro	Asn	Ser	Arg	Glu	Asn	Gly	Gly	Thr	Glu	Asn	Met	Phe	Val		
			805						810					815			
atg	tac	ctt	gga	aat	aaa	gat	gcc	tcc	cgg	gac	tac	atc	ggc	atg	gca	2496	
Met	Tyr	Leu	Gly	Asn	Lys	Asp	Ala	Ser	Arg	Asp	Tyr	Ile	Gly	Met	Ala		
			820					825					830				
gtt	gtg	gat	ggc	cag	ctc	acc	tgt	gtc	tac	aac	ctg	ggg	gac	cgt	gag	2544	
Val	Val	Asp	Gly	Gln	Leu	Thr	Cys	Val	Tyr	Asn	Leu	Gly	Asp	Arg	Glu		
		835					840					845					
gct	gaa	ctc	caa	gtg	gac	cag	atc	ttg	acc	aag	agt	gag	act	aag	gag	2592	
Ala	Glu	Leu	Gln	Val	Asp	Gln	Ile	Leu	Thr	Lys	Ser	Glu	Thr	Lys	Glu		
	850					855					860						
gca	gtt	atg	gat	cgg	gtg	aaa	ttt	cag	aga	att	tat	cag	ttt	gca	agg	2640	
Ala	Val	Met	Asp	Arg	Val	Lys	Phe	Gln	Arg	Ile	Tyr	Gln	Phe	Ala	Arg		
865					870					875					880		
ctt	aat	tac	acc	aaa	gga	gcc	aca	tcc	agt	aaa	cca	gaa	aca	ccc	gga	2688	
Leu	Asn	Tyr	Thr	Lys	Gly	Ala	Thr	Ser	Ser	Lys	Pro	Glu	Thr	Pro	Gly		
				885					890					895			
gtc	tat	gac	atg	gat	ggt	aga	aat	agc	aat	aca	ctc	ctt	aat	ttg	gat	2736	
Val	Tyr	Asp	Met	Asp	Gly	Arg	Asn	Ser	Asn	Thr	Leu	Leu	Asn	Leu	Asp		
			900					905					910				
cct	gaa	aat	gtt	gta	ttt	tat	gtt	gga	ggt	tac	cca	cct	gat	ttt	aaa	2784	
Pro	Glu	Asn	Val	Val	Phe	Tyr	Val	Gly	Gly	Tyr	Pro	Pro	Asp	Phe	Lys		
		915					920					925					
ctt	ccc	agt	cga	cta	agt	ttc	cct	cca	tac	aaa	ggt	tgt	att	gaa	tta	2832	
Leu	Pro	Ser	Arg	Leu	Ser	Phe	Pro	Pro	Tyr	Lys	Gly	Cys	Ile	Glu	Leu		
	930					935					940						
gat	gac	ctc	aat	gaa	aat	gtt	ctg	agc	ttg	tac	aac	ttc	aaa	aaa	aca	2880	
Asp	Asp	Leu	Asn	Glu	Asn	Val	Leu	Ser	Leu	Tyr	Asn	Phe	Lys	Lys	Thr		
945					950					955					960		
ttc	aat	ctc	aac	aca	act	gaa	gtg	gag	cct	tgt	aga	agg	agg	aag	gaa	2928	
Phe	Asn	Leu	Asn	Thr	Thr	Glu	Val	Glu	Pro	Cys	Arg	Arg	Arg	Lys	Glu		
				965					970					975			
gag	tca	gac	aaa	aat	tat	ttt	gaa	ggt	acg	ggc	tat	gct	cga	gtt	cca	2976	
Glu	Ser	Asp	Lys	Asn	Tyr	Phe	Glu	Gly	Thr	Gly	Tyr	Ala	Arg	Val	Pro		
			980					985					990				
act	caa	cca	cat	gct	ccc	atc	cca	acc	ttt	gga	cag	aca	att	cag	acc	3024	
Thr	Gln	Pro	His	Ala	Pro	Ile	Pro	Thr	Phe	Gly	Gln	Thr	Ile	Gln	Thr		
		995				1000						1005					
acc	gtg	gat	aga	ggc	ttg	ctg	ttc	ttt	gca	gaa	aac	ggg	gat	cgc	ttc	3072	
Thr	Val	Asp	Arg	Gly	Leu	Leu	Phe	Phe	Ala	Glu	Asn	Gly	Asp	Arg	Phe		

1010	1015	1020	
ata tct cta aat ata gaa gat ggc aag ctc atg gtg aga tac aaa ctg Ile Ser Leu Asn Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu 1025	1030	1035	3120 1040
aat tca gag cta cca aaa gag aga gga gtt gga gac gcc ata aac aac Asn Ser Glu Leu Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn 1045	1050		3168 1055
ggc aga gac cat tcg att cag atc aaa att gga aaa ctc caa aag cgt Gly Arg Asp His Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg 1060	1065	1070	3216
atg tgg ata aat gtg gac gtt caa aac act ata att gat ggt gaa gta Met Trp Ile Asn Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val 1075	1080	1085	3264
ttt gat ttc agc aca tat tat ctg gga gga att cca att gca atc agg Phe Asp Phe Ser Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg 1090	1095	1100	3312
gaa aga ttt aac att tct acg cct gct ttc cga ggc tgc atg aaa aat Glu Arg Phe Asn Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn 1105	1110	1115	3360 1120
ttg aag aaa acc agt ggt gtc gtt aga ttg aat gat act gtg gga gta Leu Lys Lys Thr Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val 1125	1130	1135	3408
acc aaa aag tgc tcg gaa gac tgg aag ctt gtg cga tct gcc tca ttc Thr Lys Lys Cys Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe 1140	1145	1150	3456
tcc aga gga gga caa ttg agt ttc act gat ttg ggc tta cca cct act Ser Arg Gly Gly Gln Leu Ser Phe Thr Asp Leu Gly Leu Pro Pro Thr 1155	1160	1165	3504
gac cac ctc cag gcc tca ttt gga ttt cag acc ttt caa ccc agt ggc Asp His Leu Gln Ala Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly 1170	1175	1180	3552
ata tta tta gat cat cag aca tgg aca agg aac ctg cag gtc act ctg Ile Leu Leu Asp His Gln Thr Trp Thr Arg Asn Leu Gln Val Thr Leu 1185	1190	1195	3600 1200
gaa gat ggt tac att gaa ttg agc acc agc gat agc ggc ggc cca att Glu Asp Gly Tyr Ile Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile 1205	1210	1215	3648
ttt aaa tct cca cag acg tat atg gat ggt tta ctg cat tat gta tct Phe Lys Ser Pro Gln Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser 1220	1225	1230	3696
gta ata agc gac aac tct gga cta cgg ctt ctc atc gat gac cag ctt Val Ile Ser Asp Asn Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu 1235	1240	1245	3744
ctg aga aat agc aaa agg cta aaa cac att tca agt tcc cgg cag tct Leu Arg Asn Ser Lys Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser 1250	1255	1260	3792

ctg cgt ctg ggc ggg agc aat ttt gag ggt tgt att agc aat gtt ttt	3840
Leu Arg Leu Gly Gly Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe	
1265 1270 1275 1280	
gtc cag agg tta tca ctg agt cct gaa gtc cta gat ttg acc agt aac	3888
Val Gln Arg Leu Ser Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn	
1285 1290 1295	
tct ctc aag aga gat gtg tcc ctg gga ggc tgc agt tta aac aaa cca	3936
Ser Leu Lys Arg Asp Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro	
1300 1305 1310	
cct ttt cta atg ttg ctt aaa ggt tct acc agg ttt aac aag acc aag	3984
Pro Phe Leu Met Leu Leu Lys Gly Ser Thr Arg Phe Asn Lys Thr Lys	
1315 1320 1325	
act ttt cgt atc aac cag ctg ttg cag gac aca cca gtg gcc tcc cca	4032
Thr Phe Arg Ile Asn Gln Leu Leu Gln Asp Thr Pro Val Ala Ser Pro	
1330 1335 1340	
agg agc gtg aag gtg tgg caa gat gct tgc tca cca ctt ccc aag acc	4080
Arg Ser Val Lys Val Trp Gln Asp Ala Cys Ser Pro Leu Pro Lys Thr	
1345 1350 1355 1360	
cag gcc aat cat gga gcc ctc cag ttt ggg gac att ccc acc agc cac	4128
Gln Ala Asn His Gly Ala Leu Gln Phe Gly Asp Ile Pro Thr Ser His	
1365 1370 1375	
ttg cta ttc aag ctt cct cag gag ctg ctg aaa ccc agg tca cag ttt	4176
Leu Leu Phe Lys Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser Gln Phe	
1380 1385 1390	
gct gtg gac atg cag aca aca tcc tcc aga gga ctg gtg ttt cac acg	4224
Ala Val Asp Met Gln Thr Thr Ser Ser Arg Gly Leu Val Phe His Thr	
1395 1400 1405	
ggc act aag aac tcc ttt atg gct ctt tat ctt tca aaa gga cgt ctg	4272
Gly Thr Lys Asn Ser Phe Met Ala Leu Tyr Leu Ser Lys Gly Arg Leu	
1410 1415 1420	
gtc ttt gca ctg ggg aca gat ggg aaa aaa ttg agg atc aaa agc aag	4320
Val Phe Ala Leu Gly Thr Asp Gly Lys Lys Leu Arg Ile Lys Ser Lys	
1425 1430 1435 1440	
gag aaa tgc aat gat ggg aaa tgg cac acg gtg gtg ttt ggc cat gat	4368
Glu Lys Cys Asn Asp Gly Lys Trp His Thr Val Val Phe Gly His Asp	
1445 1450 1455	
ggg gaa aag ggg cgc ttg gtt gtg gat gga ctg agg gcc cgg gag gga	4416
Gly Glu Lys Gly Arg Leu Val Val Asp Gly Leu Arg Ala Arg Glu Gly	
1460 1465 1470	
agt ttg cct gga aac tcc acc atc agc atc aga gcg cca gtt tac ctg	4464
Ser Leu Pro Gly Asn Ser Thr Ile Ser Ile Arg Ala Pro Val Tyr Leu	
1475 1480 1485	
gga tca cct cca tca ggg aaa cca aag agc ctc ccc aca aac agc ttt	4512
Gly S r Pro Pro Ser Gly Lys Pro Lys Ser Leu Pro Thr Asn Ser Phe	
1490 1495 1500	

gtg gga tgc ctg aag aac ttt cag ctg gat tca aaa ccc ttg tat acc 4560
 Val Gly Cys Leu Lys Asn Phe Gln Leu Asp Ser Lys Pro Leu Tyr Thr
 1505 1510 1515 1520

cct tct tca agc ttc ggg gtg tct tcc tgc ttg ggt ggt cct ttg gag 4608
 Pro Ser Ser Ser Phe Gly Val Ser Ser Cys Leu Gly Gly Pro Leu Glu
 1525 1530 1535

aaa ggc att tat ttc tct gaa gaa gga ggt cat gtc gtc ttg gct cac 4656
 Lys Gly Ile Tyr Phe Ser Glu Glu Gly Gly His Val Val Leu Ala His
 1540 1545 1550

tct gta ttg ttg ggg cca gaa ttt aag ctt gtt ttc agc atc cgc cca 4704
 Ser Val Leu Leu Gly Pro Glu Phe Lys Leu Val Phe Ser Ile Arg Pro
 1555 1560 1565

aga agt ctc act ggg atc cta ata cac atc gga agt cag ccc ggg aag 4752
 Arg Ser Leu Thr Gly Ile Leu Ile His Ile Gly Ser Gln Pro Gly Lys
 1570 1575 1580

cac tta tgt gtt tac ctg gag gca gga aag gtc acg gcc tct atg gac 4800
 His Leu Cys Val Tyr Leu Glu Ala Gly Lys Val Thr Ala Ser Met Asp
 1585 1590 1595 1600

agt ggg gca ggt ggg acc tca acg tcg gtc aca cca aag cag tct ctg 4848
 Ser Gly Ala Gly Gly Thr Ser Thr Ser Val Thr Pro Lys Gln Ser Leu
 1605 1610 1615

tgt gat gga cag tgg cac tcg gtg gca gtc acc ata aaa caa cac atc 4896
 Cys Asp Gly Gln Trp His Ser Val Ala Val Thr Ile Lys Gln His Ile
 1620 1625 1630

ctg cac ctg gaa ctg gac aca gac agt agc tac aca gct gga cag atc 4944
 Leu His Leu Glu Leu Asp Thr Asp Ser Ser Tyr Thr Ala Gly Gln Ile
 1635 1640 1645

ccc ttc cca cct gcc agc act caa gag cca cta cac ctt gga ggt gct 4992
 Pro Phe Pro Pro Ala Ser Thr Gln Glu Pro Leu His Leu Gly Gly Ala
 1650 1655 1660

cca gcc aat ttg acg aca ctg agg atc cct gtg tgg aaa tca ttc ttt 5040
 Pro Ala Asn Leu Thr Thr Leu Arg Ile Pro Val Trp Lys Ser Phe Phe
 1665 1670 1675 1680

ggc tgt ctg agg aat att cat gtc aat cac atc cct gtc cct gtc act 5088
 Gly Cys Leu Arg Asn Ile His Val Asn His Ile Pro Val Pro Val Thr
 1685 1690 1695

gaa gcc ttg gaa gtc cag ggg cct gtc agt ctg aat ggt tgt cct gac 5136
 Glu Ala Leu Glu Val Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp
 1700 1705 1710

cag taaccaagc ctatttcaca gcaaggaaat tcaccttcaa aagcactgat 5189
 Gln

tacccaatgc acctccctcc ccagctcgag atcattcttc aattaggaca caaaccagac 5249

aggtttaata gcgaatctaa ttttgaattc tgaccatgga taccatcac tttggcattc 5309

agtgctacat gtgtatttta tataaaaatc ccatttcttg aagataaaaa aattgttatt 5369

<400> 6																
Met	Gly	Trp	Leu	Trp	Ile	Phe	Gly	Ala	Ala	Leu	Gly	Gln	Cys	Leu	Gly	
1				5					10					15		
Tyr	Ser	Ser	Gln	Gln	Gln	Arg	Val	Pro	Phe	Leu	Gln	Pro	Pro	Gly	Gln	
			20					25					30			
Ser	Gln	Leu	Gln	Ala	Ser	Tyr	Val	Glu	Phe	Arg	Pro	Ser	Gln	Gly	Cys	
		35					40					45				
Ser	Pro	Gly	Tyr	Tyr	Arg	Asp	His	Lys	Gly	Leu	Tyr	Thr	Gly	Arg	Cys	
	50					55					60					
Val	Pro	Cys	Asn	Cys	Asn	Gly	His	Ser	Asn	Gln	Cys	Gln	Asp	Gly	Ser	
65					70					75					80	
Gly	Ile	Cys	Val	Asn	Cys	Gln	His	Asn	Thr	Ala	Gly	Glu	His	Cys	Glu	
				85					90					95		
Arg	Cys	Gln	Glu	Gly	Tyr	Tyr	Gly	Asn	Ala	Val	His	Gly	Ser	Cys	Arg	
			100					105					110			
Ala	Cys	Pro	Cys	Pro	His	Thr	Asn	Ser	Phe	Ala	Thr	Gly	Cys	Val	Val	
		115					120					125				
Asn	Gly	Gly	Asp	Val	Arg	Cys	Ser	Cys	Lys	Ala	Gly	Tyr	Thr	Gly	Thr	
	130					135					140					
Gln	Cys	Glu	Arg	Cys	Ala	Pro	Gly	Tyr	Phe	Gly	Asn	Pro	Gln	Lys	Phe	
145					150					155					160	
Gly	Gly	Ser	Cys	Gln	Pro	Cys	Ser	Cys	Asn	Ser	Asn	Gly	Gln	Leu	Gly	
				165					170					175		
Ser	Cys	His	Pro	Leu	Thr	Gly	Asp	Cys	Ile	Asn	Gln	Glu	Pro	Lys	Asp	
			180					185					190			
Ser	Ser	Pro	Ala	Glu	Glu	Cys	Asp	Asp	Cys	Asp	Ser	Cys	Val	Met	Thr	
		195					200					205				
Leu	Leu	Asn	Asp	Leu	Ala	Thr	Met	Gly	Glu	Gln	Leu	Arg	Leu	Val	Lys	
	210					215					220					
Ser	Gln	Leu	Gln	Gly	Leu	Ser	Ala	Ser	Ala	Gly	Leu	Leu	Glu	Gln	Met	
225					230					235					240	
Arg	His	Met	Glu	Thr	Gln	Ala	Lys	Asp	Leu	Arg	Asn	Gln	Leu	Leu	Asn	
				245					250					255		
Tyr	Arg	Ser	Ala	Ile	Ser	Asn	His	Gly	Ser	Lys	Ile	Glu	Gly	Leu	Glu	
			260					265					270			

Arg Glu Leu Thr Asp Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys
 275 280 285
 Ala Gln Val Asn Ser Arg Lys Ala Gln Thr Leu Asn Asn Asn Val Asn
 290 295 300
 Arg Ala Thr Gln Ser Ala Lys Glu Leu Asp Val Lys Ile Lys Asn Val
 305 310 315 320
 Ile Arg Asn Val His Ile Leu Leu Lys Gln Ile Ser Gly Thr Asp Gly
 325 330 335
 Glu Gly Asn Asn Val Pro Ser Gly Asp Phe Ser Arg Glu Trp Ala Glu
 340 345 350
 Ala Gln Arg Met Met Arg Glu Leu Arg Asn Arg Asn Phe Gly Lys His
 355 360 365
 Leu Arg Glu Ala Glu Ala Asp Lys Arg Glu Ser Gln Leu Leu Leu Asn
 370 375 380
 Arg Ile Arg Thr Trp Gln Lys Thr His Gln Gly Glu Asn Asn Gly Leu
 385 390 395 400
 Ala Asn Ser Ile Arg Asp Ser Leu Asn Glu Tyr Glu Ala Lys Leu Ser
 405 410 415
 Asp Leu Arg Ala Arg Leu Gln Glu Ala Ala Ala Gln Ala Lys Gln Ala
 420 425 430
 Asn Gly Leu Asn Gln Glu Asn Glu Arg Ala Leu Gly Ala Ile Gln Arg
 435 440 445
 Gln Val Lys Glu Ile Asn Ser Leu Gln Ser Asp Phe Thr Lys Tyr Leu
 450 455 460
 Thr Thr Ala Asp Ser Ser Leu Leu Gln Thr Asn Ile Ala Leu Gln Leu
 465 470 475 480
 Met Glu Lys Ser Gln Lys Glu Tyr Glu Lys Leu Ala Ala Ser Leu Asn
 485 490 495
 Glu Ala Arg Gln Glu Leu Ser Asp Lys Val Arg Glu Leu Ser Arg Ser
 500 505 510
 Ala Gly Lys Thr Ser Leu Val Glu Glu Ala Glu Lys His Ala Arg Ser
 515 520 525
 Leu Gln Glu Leu Ala Lys Gln Leu Glu Glu Ile Lys Arg Asn Ala Ser
 530 535 540
 Gly Asp Glu Leu Val Arg Cys Ala Val Asp Ala Ala Thr Ala Tyr Glu
 545 550 555 560
 Asn Ile Leu Asn Ala Ile Lys Ala Ala Glu Asp Ala Ala Asn Arg Ala
 565 570 575
 Ala Ser Ala Ser Glu Ser Ala L u Gln Thr Val Ile Lys Glu Asp Leu
 580 585 590

Pro Arg Lys Ala Lys Thr Leu Ser Ser Asn Ser Asp Lys Leu Leu Asn
 595 600 605
 Glu Ala Lys Met Thr Gln Lys Lys Leu Lys Gln Glu Val Ser Pro Ala
 610 615 620
 Leu Asn Asn Leu Gln Gln Thr Leu Asn Ile Val Thr Val Gln Lys Glu
 625 630 635 640
 Val Ile Asp Thr Asn Leu Thr Thr Leu Arg Asp Gly Leu His Gly Ile
 645 650 655
 Gln Arg Gly Asp Ile Asp Ala Met Ile Ser Ser Ala Lys Ser Met Val
 660 665 670
 Arg Lys Ala Asn Asp Ile Thr Asp Glu Val Leu Asp Gly Leu Asn Pro
 675 680 685
 Ile Gln Thr Asp Val Glu Arg Ile Lys Asp Thr Tyr Gly Arg Thr Gln
 690 695 700
 Asn Glu Asp Phe Lys Lys Ala Leu Thr Asp Ala Asp Asn Ser Val Asn
 705 710 715 720
 Lys Leu Thr Asn Lys Leu Pro Asp Leu Trp Arg Lys Ile Glu Ser Ile
 725 730 735
 Asn Gln Gln Leu Leu Pro Leu Gly Asn Ile Ser Asp Asn Met Asp Arg
 740 745 750
 Ile Arg Glu Leu Ile Gln Gln Ala Arg Asp Ala Ala Ser Lys Val Ala
 755 760 765
 Val Pro Met Arg Phe Asn Gly Lys Ser Gly Val Glu Val Arg Leu Pro
 770 775 780
 Asn Asp Leu Glu Asp Leu Lys Gly Tyr Thr Ser Leu Ser Leu Phe Leu
 785 790 795 800
 Gln Arg Pro Asn Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val
 805 810 815
 Met Tyr Leu Gly Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala
 820 825 830
 Val Val Asp Gly Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu
 835 840 845
 Ala Glu Leu Gln Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu
 850 855 860
 Ala Val Met Asp Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg
 865 870 875 880
 Leu Asn Tyr Thr Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly
 885 890 895
 Val Tyr Asp Met Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp
 900 905 910
 Pro Glu Asn Val Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys

915	920	925
Leu Pro Ser Arg Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu		
930	935	940
Asp Asp Leu Asn Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr		
945	950	955
		960
Phe Asn Leu Asn Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu		
	965	970
		975
Glu Ser Asp Lys Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro		
	980	985
		990
Thr Gln Pro His Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr		
	995	1000
		1005
Thr Val Asp Arg Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe		
	1010	1015
		1020
Ile Ser Leu Asn Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu		
1025	1030	1035
		1040
Asn Ser Glu Leu Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn		
	1045	1050
		1055
Gly Arg Asp His Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg		
	1060	1065
		1070
Met Trp Ile Asn Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val		
	1075	1080
		1085
Phe Asp Phe Ser Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg		
	1090	1095
		1100
Glu Arg Phe Asn Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn		
1105	1110	1115
		1120
Leu Lys Lys Thr Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val		
	1125	1130
		1135
Thr Lys Lys Cys Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe		
	1140	1145
		1150
Ser Arg Gly Gly Gln Leu Ser Phe Thr Asp Leu Gly Leu Pro Pro Thr		
	1155	1160
		1165
Asp His Leu Gln Ala Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly		
1170	1175	1180
Ile Leu Leu Asp His Gln Thr Trp Thr Arg Asn Leu Gln Val Thr Leu		
1185	1190	1195
		1200
Glu Asp Gly Tyr Ile Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile		
	1205	1210
		1215
Phe Lys Ser Pro Gln Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser		
	1220	1225
		1230
Val Ile Ser Asp Asn Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu		
1235	1240	1245

Leu Arg Asn Ser Lys Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser
1250 1255 1260

Leu Arg Leu Gly Gly Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe
1265 1270 1275 1280

Val Gln Arg Leu Ser Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn
1285 1290 1295

Ser Leu Lys Arg Asp Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro
1300 1305 1310

Pro Phe Leu Met Leu Leu Lys Gly Ser Thr Arg Phe Asn Lys Thr Lys
1315 1320 1325

Thr Phe Arg Ile Asn Gln Leu Leu Gln Asp Thr Pro Val Ala Ser Pro
1330 1335 1340

Arg Ser Val Lys Val Trp Gln Asp Ala Cys Ser Pro Leu Pro Lys Thr
1345 1350 1355 1360

Gln Ala Asn His Gly Ala Leu Gln Phe Gly Asp Ile Pro Thr Ser His
1365 1370 1375

Leu Leu Phe Lys Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser Gln Phe
1380 1385 1390

Ala Val Asp Met Gln Thr Thr Ser Ser Arg Gly Leu Val Phe His Thr
1395 1400 1405

Gly Thr Lys Asn Ser Phe Met Ala Leu Tyr Leu Ser Lys Gly Arg Leu
1410 1415 1420

Val Phe Ala Leu Gly Thr Asp Gly Lys Lys Leu Arg Ile Lys Ser Lys
1425 1430 1435 1440

Glu Lys Cys Asn Asp Gly Lys Trp His Thr Val Val Phe Gly His Asp
1445 1450 1455

Gly Glu Lys Gly Arg Leu Val Val Asp Gly Leu Arg Ala Arg Glu Gly
1460 1465 1470

Ser Leu Pro Gly Asn Ser Thr Ile Ser Ile Arg Ala Pro Val Tyr Leu
1475 1480 1485

Gly Ser Pro Pro Ser Gly Lys Pro Lys Ser Leu Pro Thr Asn Ser Phe
1490 1495 1500

Val Gly Cys Leu Lys Asn Phe Gln Leu Asp Ser Lys Pro Leu Tyr Thr
1505 1510 1515 1520

Pro Ser Ser Ser Phe Gly Val Ser Ser Cys Leu Gly Gly Pro Leu Glu
1525 1530 1535

Lys Gly Ile Tyr Phe Ser Glu Glu Gly Gly His Val Val Leu Ala His
1540 1545 1550

Ser Val Leu Leu Gly Pro Glu Phe Lys Leu Val Phe Ser Ile Arg Pro
1555 1560 1565

Arg Ser Leu Thr Gly Ile Leu Ile His Ile Gly Ser Gln Pro Gly Lys
 1570 1575 1580
 His Leu Cys Val Tyr Leu Glu Ala Gly Lys Val Thr Ala Ser Met Asp
 1585 1590 1595 1600
 Ser Gly Ala Gly Gly Thr Ser Thr Ser Val Thr Pro Lys Gln Ser Leu
 1605 1610 1615
 Cys Asp Gly Gln Trp His Ser Val Ala Val Thr Ile Lys Gln His Ile
 1620 1625 1630
 Leu His Leu Glu Leu Asp Thr Asp Ser Ser Tyr Thr Ala Gly Gln Ile
 1635 1640 1645
 Pro Phe Pro Pro Ala Ser Thr Gln Glu Pro Leu His Leu Gly Gly Ala
 1650 1655 1660
 Pro Ala Asn Leu Thr Thr Leu Arg Ile Pro Val Trp Lys Ser Phe Phe
 1665 1670 1675 1680
 Gly Cys Leu Arg Asn Ile His Val Asn His Ile Pro Val Pro Val Thr
 1685 1690 1695
 Glu Ala Leu Glu Val Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp
 1700 1705 1710

Gln

<210> 7
 <211> 5373
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(5079)

<400> 7
 cag caa agg gtg cca ttt ctt cag cct ccc ggt caa agt caa ctg caa 48
 Gln Gln Arg Val Pro Phe Leu Gln Pro Pro Gly Gln Ser Gln Leu Gln
 1 5 10 15
 gcg agt tat gtg gag ttt aga ccc agc cag ggt tgt agc cct gga tac 96
 Ala Ser Tyr Val Glu Phe Arg Pro Ser Gln Gly Cys Ser Pro Gly Tyr
 20 25 30
 tat cgg gat cat aaa ggc ttg tat acc gga cgg tgt gtt ccc tgc aat 144
 Tyr Arg Asp His Lys Gly Leu Tyr Thr Gly Arg Cys Val Pro Cys Asn
 35 40 45
 tgc aac gga cat tca aat caa tgc cag gat ggc tca ggc ata tgt gtt 192
 Cys Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser Gly Ile Cys Val
 50 55 60
 aac tgt cag cac aac acc gcg gga gag cac tgt gaa cgc tgc cag gag 240
 Asn Cys Gln His Asn Thr Ala Gly Glu His Cys Glu Arg Cys Gln Glu
 65 70 75 80

ggc tac tat ggc aac gcc gtc cac gga tcc tgc agg gcc tgc cca tgt	288
Gly Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg Ala Cys Pro Cys	
85 90 95	
cct cac act aac agc ttt gcc act ggc tgt gtg gtg aat ggg gga gac	336
Pro His Thr Asn Ser Phe Ala Thr Gly Cys Val Val Asn Gly Gly Asp	
100 105 110	
gtg cgg tgc tcc tgc aaa gct ggg tac aca gga aca cag tgt gaa agg	384
Val Arg Cys Ser Cys Lys Ala Gly Tyr Thr Gly Thr Gln Cys Glu Arg	
115 120 125	
tgt gca ccg gga tat ttc ggg aat ccc cag aaa ttc gga ggt agc tgc	432
Cys Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe Gly Gly Ser Cys	
130 135 140	
caa cca tgc agt tgt aac agc aat ggc cag ctg ggc agc tgt cat ccc	480
Gln Pro Cys Ser Cys Asn Ser Asn Gly Gln Leu Gly Ser Cys His Pro	
145 150 155 160	
ctg act gga gac tgc ata aac caa gaa ccc aaa gat agc agc cct gca	528
Leu Thr Gly Asp Cys Ile Asn Gln Glu Pro Lys Asp Ser Ser Pro Ala	
165 170 175	
gaa gaa tgt gat gat tgc gac agc tgt gtg atg acc ctc ctg aac gac	576
Glu Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr Leu Leu Asn Asp	
180 185 190	
ctg gcc acc atg ggc gag cag ctc cgc ctg gtc aag tct cag ctg cag	624
Leu Ala Thr Met Gly Glu Gln Leu Arg Leu Val Lys Ser Gln Leu Gln	
195 200 205	
ggc ctg agt gcc agc gca ggg ctt ctg gag cag atg agg cac atg gag	672
Gly Leu Ser Ala Ser Ala Gly Leu Leu Glu Gln Met Arg His Met Glu	
210 215 220	
acc cag gcc aag gac ctg agg aat cag ttg ctc aac tac cgt tct gcc	720
Thr Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Asn Tyr Arg Ser Ala	
225 230 235 240	
att tca aat cat gga tca aaa ata gaa ggc ctg gaa aga gaa ctg act	768
Ile Ser Asn His Gly Ser Lys Ile Glu Gly Leu Glu Arg Glu Leu Thr	
245 250 255	
gat ttg aat caa gaa ttt gag act ttg caa gaa aag gct caa gta aat	816
Asp Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys Ala Gln Val Asn	
260 265 270	
tcc aga aaa gca caa aca tta aac aac aat gtt aat cgg gca aca caa	864
Ser Arg Lys Ala Gln Thr Leu Asn Asn Asn Val Asn Arg Ala Thr Gln	
275 280 285	
agc gca aaa gaa ctg gat gtg aag att aaa aat gtc atc cgg aat gtg	912
Ser Ala Lys Glu Leu Asp Val Lys Ile Lys Asn Val Ile Arg Asn Val	
290 295 300	
cac att ctt tta aag cag atc tct ggg aca gat gga gag gga aac aac	960
His Ile Leu Leu Lys Gln Ile Ser Gly Thr Asp Gly Glu Gly Asn Asn	
305 310 315 320	
gtg cct tca ggt gac ttt tcc aga gag tgg gct gaa gcc cag cgc atg	1008

Val	Pro	Ser	Gly	Asp	Phe	Ser	Arg	Glu	Trp	Ala	Glu	Ala	Gln	Arg	Met	
				325					330					335		
atg	agg	gaa	ctg	cgg	aac	agg	aac	ttt	gga	aag	cac	ctc	aga	gaa	gca	1056
Met	Arg	Glu	Leu	Arg	Asn	Arg	Asn	Phe	Gly	Lys	His	Leu	Arg	Glu	Ala	
			340					345					350			
gaa	gct	gat	aaa	agg	gag	tcg	cag	ctc	ttg	ctg	aac	cgg	ata	agg	acc	1104
Glu	Ala	Asp	Lys	Arg	Glu	Ser	Gln	Leu	Leu	Leu	Asn	Arg	Ile	Arg	Thr	
			355				360					365				
tgg	cag	aaa	acc	cac	cag	ggg	gag	aac	aat	ggg	ctt	gct	aac	agt	atc	1152
Trp	Gln	Lys	Thr	His	Gln	Gly	Glu	Asn	Asn	Gly	Leu	Ala	Asn	Ser	Ile	
	370					375					380					
cgg	gat	tct	tta	aat	gaa	tac	gaa	gcc	aaa	ctc	agt	gac	ctt	cgt	gct	1200
Arg	Asp	Ser	Leu	Asn	Glu	Tyr	Glu	Ala	Lys	Leu	Ser	Asp	Leu	Arg	Ala	
	385				390					395					400	
cgg	ctg	cag	gag	gca	gct	gcc	caa	gcc	aag	cag	gca	aat	ggc	ttg	aac	1248
Arg	Leu	Gln	Glu	Ala	Ala	Ala	Gln	Ala	Lys	Gln	Ala	Asn	Gly	Leu	Asn	
				405					410					415		
caa	gaa	aac	gag	aga	gct	ttg	gga	gcc	att	cag	aga	caa	gtg	aaa	gaa	1296
Gln	Glu	Asn	Glu	Arg	Ala	Leu	Gly	Ala	Ile	Gln	Arg	Gln	Val	Lys	Glu	
			420					425					430			
ata	aat	tcc	ctg	cag	agt	gat	ttc	acc	aag	tat	cta	acc	act	gca	gac	1344
Ile	Asn	Ser	Leu	Gln	Ser	Asp	Phe	Thr	Lys	Tyr	Leu	Thr	Thr	Ala	Asp	
			435				440					445				
tca	tct	ttg	ttg	caa	acc	aac	att	gcg	ctg	cag	ctg	atg	gag	aaa	agc	1392
Ser	Ser	Leu	Leu	Gln	Thr	Asn	Ile	Ala	Leu	Gln	Leu	Met	Glu	Lys	Ser	
		450				455					460					
cag	aag	gaa	tat	gaa	aaa	tta	gct	gcc	agt	tta	aat	gaa	gca	aga	caa	1440
Gln	Lys	Glu	Tyr	Glu	Lys	Leu	Ala	Ala	Ser	Leu	Asn	Glu	Ala	Arg	Gln	
					470					475					480	
gaa	cta	agt	gac	aaa	gta	aga	gaa	ctt	tcc	aga	tct	gct	ggc	aaa	aca	1488
Glu	Leu	Ser	Asp	Lys	Val	Arg	Glu	Leu	Ser	Arg	Ser	Ala	Gly	Lys	Thr	
				485					490					495		
tcc	ctt	gtg	gag	gag	gca	gaa	aag	cac	gcg	cgg	tcc	tta	caa	gag	ctg	1536
Ser	Leu	Val	Glu	Glu	Ala	Glu	Lys	His	Ala	Arg	Ser	Leu	Gln	Glu	Leu	
			500					505					510			
gca	aag	cag	ctg	gaa	gag	atc	aag	aga	aac	gcc	agc	ggg	gat	gag	ctg	1584
Ala	Lys	Gln	Leu	Glu	Glu	Ile	Lys	Arg	Asn	Ala	Ser	Gly	Asp	Glu	Leu	
			515				520					525				
gtg	cgc	tgt	gct	gtg	gat	gcc	gcc	acc	gcc	tac	gag	aac	atc	ctc	aat	1632
Val	Arg	Cys	Ala	Val	Asp	Ala	Ala	Thr	Ala	Tyr	Glu	Asn	Ile	Leu	Asn	
			530			535					540					
gcc	atc	aaa	gcg	gcc	gag	gac	gca	gcc	aac	agg	gct	gcc	agt	gca	tct	1680
Ala	Ile	Lys	Ala	Ala	Glu	Asp	Ala	Ala	Asn	Arg	Ala	Ala	Ser	Ala	Ser	
					545		550			555					560	
gaa	tct	gcc	ctc	cag	aca	gtg	ata	aag	gaa	gat	ctg	cca	aga	aaa	gct	1728
Glu	Ser	Ala	Leu	Gln	Thr	Val	Ile	Lys	Glu	Asp	Leu	Pro	Arg	Lys	Ala	

565								570								575								
aaa	acc	ctg	agt	tcc	aac	agt	gat	aaa	ctg	tta	aat	gaa	gcc	aag	atg	1776								
Lys	Thr	Leu	Ser	Ser	Asn	Ser	Asp	Lys	Leu	Leu	Asn	Glu	Ala	Lys	Met									
			580						585				590											
aca	caa	aag	aag	cta	aag	caa	gaa	gtc	agt	cca	gct	ctc	aac	aac	cta	1824								
Thr	Gln	Lys	Lys	Leu	Lys	Gln	Glu	Val	Ser	Pro	Ala	Leu	Asn	Asn	Leu									
		595					600					605												
cag	caa	acc	ctg	aat	att	gtg	aca	ggt	cag	aaa	gaa	gtg	ata	gac	acc	1872								
Gln	Gln	Thr	Leu	Asn	Ile	Val	Thr	Val	Gln	Lys	Glu	Val	Ile	Asp	Thr									
		610				615					620													
aat	ctc	aca	act	ctc	cga	gat	ggg	ctt	cat	ggg	ata	cag	aga	ggg	gat	1920								
Asn	Leu	Thr	Thr	Leu	Arg	Asp	Gly	Leu	His	Gly	Ile	Gln	Arg	Gly	Asp									
					630					635				640										
att	gat	gct	atg	atc	agt	agt	gca	aag	agc	atg	gtc	aga	aag	gcc	aac	1968								
Ile	Asp	Ala	Met	Ile	Ser	Ser	Ala	Lys	Ser	Met	Val	Arg	Lys	Ala	Asn									
				645					650					655										
gac	atc	aca	gat	gag	gtt	ctg	gat	ggg	ctc	aac	ccc	atc	cag	aca	gat	2016								
Asp	Ile	Thr	Asp	Glu	Val	Leu	Asp	Gly	Leu	Asn	Pro	Ile	Gln	Thr	Asp									
			660				665					670												
gtg	gaa	aga	att	aag	gac	acc	tat	ggg	agg	aca	cag	aac	gaa	gac	ttc	2064								
Val	Glu	Arg	Ile	Lys	Asp	Thr	Tyr	Gly	Arg	Thr	Gln	Asn	Glu	Asp	Phe									
		675					680				685													
aaa	aag	gct	ctg	act	gat	gca	gat	aac	tcg	gtg	aat	aag	tta	acc	aac	2112								
Lys	Lys	Ala	Leu	Thr	Asp	Ala	Asp	Asn	Ser	Val	Asn	Lys	Leu	Thr	Asn									
		690				695					700													
aaa	cta	cct	gat	ctt	tgg	cgc	aag	att	gaa	agt	atc	aac	caa	cag	ctg	2160								
Lys	Leu	Pro	Asp	Leu	Trp	Arg	Lys	Ile	Glu	Ser	Ile	Asn	Gln	Gln	Leu									
					710					715				720										
ttg	ccc	ttg	gga	aac	atc	tct	gac	aac	atg	gac	aga	ata	cga	gaa	cta	2208								
Leu	Pro	Leu	Gly	Asn	Ile	Ser	Asp	Asn	Met	Asp	Arg	Ile	Arg	Glu	Leu									
				725					730					735										
att	cag	cag	gcc	aga	gat	gct	gcc	agt	aag	ggt	gct	gtc	ccc	atg	agg	2256								
Ile	Gln	Gln	Ala	Arg	Asp	Ala	Ala	Ser	Lys	Val	Ala	Val	Pro	Met	Arg									
			740				745						750											
ttc	aat	ggg	aaa	tct	gga	gtc	gaa	gtc	cga	ctg	cca	aat	gac	ctg	gaa	2304								
Phe	Asn	Gly	Lys	Ser	Gly	Val	Glu	Val	Arg	Leu	Pro	Asn	Asp	Leu	Glu									
		755				760					765													
gat	ttg	aaa	gga	tat	aca	tct	ctg	tcc	ttg	ttt	ctc	caa	agg	ccc	aac	2352								
Asp	Leu	Lys	Gly	Tyr	Thr	Ser	Leu	Ser	Leu	Phe	Leu	Gln	Arg	Pro	Asn									
		770				775					780													
tca	aga	gaa	aat	ggg	ggg	act	gag	aat	atg	ttt	gtg	atg	tac	ctt	gga	2400								
Ser	Arg	Glu	Asn	Gly	Gly	Thr	Glu	Asn	Met	Phe	Val	Met	Tyr	Leu	Gly									
		785			790				795					800										
aat	aaa	gat	gcc	tcc	cgg	gac	tac	atc	ggc	atg	gca	ggt	gtg	gat	ggc	2448								
Asn	Lys	Asp	Ala	Ser	Arg	Asp	Tyr	Ile	Gly	Met	Ala	Val	Val	Asp	Gly									
			805						810					815										

cag ctc acc tgt gtc tac aac ctg ggg gac cgt gag gct gaa ctc caa	2496
Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu Leu Gln	
820 825 830	
gtg gac cag atc ttg acc aag agt gag act aag gag gca gtt atg gat	2544
Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val Met Asp	
835 840 845	
cgg gtg aaa ttt cag aga att tat cag ttt gca agg ctt aat tac acc	2592
Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn Tyr Thr	
850 855 860	
aaa gga gcc aca tcc agt aaa cca gaa aca ccc gga gtc tat gac atg	2640
Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr Asp Met	
865 870 875 880	
gat ggt aga aat agc aat aca ctc ctt aat ttg gat cct gaa aat gtt	2688
Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu Asn Val	
885 890 895	
gta ttt tat gtt gga ggt tac cca cct gat ttt aaa ctt ccc agt cga	2736
Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro Ser Arg	
900 905 910	
cta agt ttc cct cca tac aaa ggt tgt att gaa tta gat gac ctc aat	2784
Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp Leu Asn	
915 920 925	
gaa aat gtt ctg agc ttg tac aac ttc aaa aaa aca ttc aat ctc aac	2832
Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn Leu Asn	
930 935 940	
aca act gaa gtg gag cct tgt aga agg agg aag gaa gag tca gac aaa	2880
Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser Asp Lys	
945 950 955 960	
aat tat ttt gaa ggt acg ggc tat gct cga gtt cca act caa cca cat	2928
Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln Pro His	
965 970 975	
gct ccc atc cca acc ttt gga cag aca att cag acc acc gtg gat aga	2976
Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val Asp Arg	
980 985 990	
ggc ttg ctg ttc ttt gca gaa aac ggg gat cgc ttc ata tct cta aat	3024
Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Ile Ser Leu Asn	
995 1000 1005	
ata gaa gat ggc aag ctc atg gtg aga tac aaa ctg aat tca gag cta	3072
Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser Glu Leu	
1010 1015 1020	
cca aaa gag aga gga gtt gga gac gcc ata aac aac ggc aga gac cat	3120
Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg Asp His	
1025 1030 1035 1040	
tcg att cag atc aaa att gga aaa ctc caa aag cgt atg tgg ata aat	3168
Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp Ile Asn	
1045 1050 1055	

gtg gac gtt caa aac act ata att gat ggt gaa gta ttt gat ttc agc	3216
Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp Phe Ser	
1060 1065 1070	
aca tat tat ctg gga gga att cca att gca atc agg gaa aga ttt aac	3264
Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg Phe Asn	
1075 1080 1085	
att tct acg cct gct ttc cga ggc tgc atg aaa aat ttg aag aaa acc	3312
Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys Lys Thr	
1090 1095 1100	
agt ggt gtc gtt aga ttg aat gat act gtg gga gta acc aaa aag tgc	3360
Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys Lys Cys	
1105 1110 1115 1120	
tcg gaa gac tgg aag ctt gtg cga tct gcc tca ttc tcc aga gga gga	3408
Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg Gly Gly	
1125 1130 1135	
caa ttg agt ttc act gat ttg ggc tta cca cct act gac cac ctc cag	3456
Gln Leu Ser Phe Thr Asp Leu Gly Leu Pro Pro Thr Asp His Leu Gln	
1140 1145 1150	
gcc tca ttt gga ttt cag acc ttt caa ccc agt ggc ata tta tta gat	3504
Ala Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly Ile Leu Leu Asp	
1155 1160 1165	
cat cag aca tgg aca agg aac ctg cag gtc act ctg gaa gat ggt tac	3552
His Gln Thr Trp Thr Arg Asn Leu Gln Val Thr Leu Glu Asp Gly Tyr	
1170 1175 1180	
att gaa ttg agc acc agc gat agc ggc ggc cca att ttt aaa tct cca	3600
Ile Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile Phe Lys Ser Pro	
1185 1190 1195 1200	
cag acg tat atg gat ggt tta ctg cat tat gta tct gta ata agc gac	3648
Gln Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser Val Ile Ser Asp	
1205 1210 1215	
aac tct gga cta cgg ctt ctc atc gat gac cag ctt ctg aga aat agc	3696
Asn Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu Leu Arg Asn Ser	
1220 1225 1230	
aaa agg cta aaa cac att tca agt tcc cgg cag tct ctg cgt ctg ggc	3744
Lys Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser Leu Arg Leu Gly	
1235 1240 1245	
ggg agc aat ttt gag ggt tgt att agc aat gtt ttt gtc cag agg tta	3792
Gly Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe Val Gln Arg Leu	
1250 1255 1260	
tca ctg agt cct gaa gtc cta gat ttg acc agt aac tct ctc aag aga	3840
Ser Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn Ser Leu Lys Arg	
1265 1270 1275 1280	
gat gtg tcc ctg gga ggc tgc agt tta aac aaa cca cct ttt cta atg	3888
Asp Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe Leu Met	
1285 1290 1295	
ttg ctt aaa ggt tct acc agg ttt aac aag acc aag act ttt cgt atc	3936

Leu	Leu	Lys	Gly	Ser	Thr	Arg	Phe	Asn	Lys	Thr	Lys	Thr	Phe	Arg	Ile	
			1300					1305						1310		
aac	cag	ctg	ttg	cag	gac	aca	cca	gtg	gcc	tcc	cca	agg	agc	gtg	aag	3984
Asn	Gln	Leu	Leu	Gln	Asp	Thr	Pro	Val	Ala	Ser	Pro	Arg	Ser	Val	Lys	
		1315					1320				1325					
gtg	tgg	caa	gat	gct	tgc	tca	cca	ctt	ccc	aag	acc	cag	gcc	aat	cat	4032
Val	Trp	Gln	Asp	Ala	Cys	Ser	Pro	Leu	Pro	Lys	Thr	Gln	Ala	Asn	His	
		1330				1335					1340					
gga	gcc	ctc	cag	ttt	ggg	gac	att	ccc	acc	agc	cac	ttg	cta	ttc	aag	4080
Gly	Ala	Leu	Gln	Phe	Gly	Asp	Ile	Pro	Thr	Ser	His	Leu	Leu	Phe	Lys	
		1345			1350					1355					1360	
ctt	cct	cag	gag	ctg	ctg	aaa	ccc	agg	tca	cag	ttt	gct	gtg	gac	atg	4128
Leu	Pro	Gln	Glu	Leu	Leu	Lys	Pro	Arg	Ser	Gln	Phe	Ala	Val	Asp	Met	
			1365					1370						1375		
cag	aca	aca	tcc	tcc	aga	gga	ctg	gtg	ttt	cac	acg	ggc	act	aag	aac	4176
Gln	Thr	Thr	Ser	Ser	Arg	Gly	Leu	Val	Phe	His	Thr	Gly	Thr	Lys	Asn	
			1380				1385						1390			
tcc	ttt	atg	gct	ctt	tat	ctt	tca	aaa	gga	cgt	ctg	gtc	ttt	gca	ctg	4224
Ser	Phe	Met	Ala	Leu	Tyr	Leu	Ser	Lys	Gly	Arg	Leu	Val	Phe	Ala	Leu	
		1395					1400					1405				
ggg	aca	gat	ggg	aaa	aaa	ttg	agg	atc	aaa	agc	aag	gag	aaa	tgc	aat	4272
Gly	Thr	Asp	Gly	Lys	Lys	Leu	Arg	Ile	Lys	Ser	Lys	Glu	Lys	Cys	Asn	
		1410				1415					1420					
gat	ggg	aaa	tgg	cac	acg	gtg	gtg	ttt	ggc	cat	gat	ggg	gaa	aag	ggg	4320
Asp	Gly	Lys	Trp	His	Thr	Val	Val	Phe	Gly	His	Asp	Gly	Glu	Lys	Gly	
		1425			1430				1435					1440		
cgc	ttg	gtt	gtg	gat	gga	ctg	agg	gcc	cgg	gag	gga	agt	ttg	cct	gga	4368
Arg	Leu	Val	Val	Asp	Gly	Leu	Arg	Ala	Arg	Glu	Gly	Ser	Leu	Pro	Gly	
			1445					1450						1455		
aac	tcc	acc	atc	agc	atc	aga	gcg	cca	gtt	tac	ctg	gga	tca	cct	cca	4416
Asn	Ser	Thr	Ile	Ser	Ile	Arg	Ala	Pro	Val	Tyr	Leu	Gly	Ser	Pro	Pro	
			1460					1465					1470			
tca	ggg	aaa	cca	aag	agc	ctc	ccc	aca	aac	agc	ttt	gtg	gga	tgc	ctg	4464
Ser	Gly	Lys	Pro	Lys	Ser	Leu	Pro	Thr	Asn	Ser	Phe	Val	Gly	Cys	Leu	
		1475					1480					1485				
aag	aac	ttt	cag	ctg	gat	tca	aaa	ccc	ttg	tat	acc	cct	tct	tca	agc	4512
Lys	Asn	Phe	Gln	Leu	Asp	Ser	Lys	Pro	Leu	Tyr	Thr	Pro	Ser	Ser	Ser	
		1490				1495					1500					
ttc	ggg	gtg	tct	tcc	tgc	ttg	ggg	ggg	cct	ttg	gag	aaa	ggc	att	tat	4560
Phe	Gly	Val	Ser	Ser	Cys	Leu	Gly	Gly	Pro	Leu	Glu	Lys	Gly	Ile	Tyr	
		1505			1510				1515					1520		
ttc	tct	gaa	gaa	gga	ggg	cat	gtc	gtc	ttg	gct	cac	tct	gta	ttg	ttg	4608
Phe	Ser	Glu	Glu	Gly	Gly	His	Val	Val	Leu	Ala	His	Ser	Val	Leu	Leu	
			1525					1530						1535		
ggg	cca	gaa	ttt	aag	ctt	gtt	ttc	agc	atc	cgc	cca	aga	agt	ctc	act	4656
Gly	Pro	Glu	Phe	Lys	Leu	Val	Phe	Ser	Ile	Arg	Pro	Arg	Ser	Leu	Thr	

1540 1545 1550

ggg atc cta ata cac atc gga agt cag ccc ggg aag cac tta tgt gtt 4704
Gly Ile Leu Ile His Ile Gly Ser Gln Pro Gly Lys His Leu Cys Val
1555 1560 1565

tac ctg gag gca gga aag gtc acg gcc tct atg gac agt ggg gca ggt 4752
Tyr Leu Glu Ala Gly Lys Val Thr Ala Ser Met Asp Ser Gly Ala Gly
1570 1575 1580

ggg acc tca acg tcg gtc aca cca aag cag tct ctg tgt gat gga cag 4800
Gly Thr Ser Thr Ser Val Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln
1585 1590 1595 1600

tgg cac tcg gtg gca gtc acc ata aaa caa cac atc ctg cac ctg gaa 4848
Trp His Ser Val Ala Val Thr Ile Lys Gln His Ile Leu His Leu Glu
1605 1610 1615

ctg gac aca gac agt agc tac aca gct gga cag atc ccc ttc cca cct 4896
Leu Asp Thr Asp Ser Ser Tyr Thr Ala Gly Gln Ile Pro Phe Pro Pro
1620 1625 1630

gcc agc act caa gag cca cta cac ctt gga ggt gct cca gcc aat ttg 4944
Ala Ser Thr Gln Glu Pro Leu His Leu Gly Gly Ala Pro Ala Asn Leu
1635 1640 1645

acg aca ctg agg atc cct gtg tgg aaa tca ttc ttt ggc tgt ctg agg 4992
Thr Thr Leu Arg Ile Pro Val Trp Lys Ser Phe Phe Gly Cys Leu Arg
1650 1655 1660

aat att cat gtc aat cac atc cct gtc cct gtc act gaa gcc ttg gaa 5040
Asn Ile His Val Asn His Ile Pro Val Pro Val Thr Glu Ala Leu Glu
1665 1670 1675 1680

gtc cag ggg cct gtc agt ctg aat ggt tgt cct gac cag taacccaagc 5089
Val Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp Gln
1685 1690

ctatttcaca gcaaggaaat tcaccttcaa aagcactgat tacccaatgc acctccctcc 5149

ccagctcgag atcattcttc aattaggaca caaaccagac aggtttaata gcgaatctaa 5209

ttttgaattc tgaccatgga taccatcac tttggcattc agtgctacat gtgtatttta 5269

tataaaaatc ccatttcttg aagataaaaa aattgttatt caaattgtta tgcacagaat 5329

gtttttggta atattaattt ccactaaaaa attaatgtc tttt 5373

<210> 8
<211> 1693
<212> PRT
<213> Homo sapiens

<400> 8
Gln Gln Arg Val Pro Phe Leu Gln Pro Pro Gly Gln Ser Gln Leu Gln
1 5 10 15
Ala Ser Tyr Val Glu Phe Arg Pro Ser Gln Gly Cys Ser Pro Gly Tyr
20 25 30

Tyr Arg Asp His Lys Gly Leu Tyr Thr Gly Arg Cys Val Pro Cys Asn
35 40 45

Cys Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser Gly Ile Cys Val
50 55 60

Asn Cys Gln His Asn Thr Ala Gly Glu His Cys Glu Arg Cys Gln Glu
65 70 75 80

Gly Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg Ala Cys Pro Cys
85 90 95

Pro His Thr Asn Ser Phe Ala Thr Gly Cys Val Val Asn Gly Gly Asp
100 105 110

Val Arg Cys Ser Cys Lys Ala Gly Tyr Thr Gly Thr Gln Cys Glu Arg
115 120 125

Cys Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe Gly Gly Ser Cys
130 135 140

Gln Pro Cys Ser Cys Asn Ser Asn Gly Gln Leu Gly Ser Cys His Pro
145 150 155 160

Leu Thr Gly Asp Cys Ile Asn Gln Glu Pro Lys Asp Ser Ser Pro Ala
165 170 175

Glu Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr Leu Leu Asn Asp
180 185 190

Leu Ala Thr Met Gly Glu Gln Leu Arg Leu Val Lys Ser Gln Leu Gln
195 200 205

Gly Leu Ser Ala Ser Ala Gly Leu Leu Glu Gln Met Arg His Met Glu
210 215 220

Thr Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Asn Tyr Arg Ser Ala
225 230 235 240

Ile Ser Asn His Gly Ser Lys Ile Glu Gly Leu Glu Arg Glu Leu Thr
245 250 255

Asp Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys Ala Gln Val Asn
260 265 270

Ser Arg Lys Ala Gln Thr Leu Asn Asn Asn Val Asn Arg Ala Thr Gln
275 280 285

Ser Ala Lys Glu Leu Asp Val Lys Ile Lys Asn Val Ile Arg Asn Val
290 295 300

His Ile Leu Leu Lys Gln Ile Ser Gly Thr Asp Gly Glu Gly Asn Asn
305 310 315 320

Val Pro Ser Gly Asp Phe Ser Arg Glu Trp Ala Glu Ala Gln Arg Met
325 330 335

Met Arg Glu Leu Arg Asn Arg Asn Phe Gly Lys His Leu Arg Glu Ala
340 345 350

Glu Ala Asp Lys Arg Glu Ser Gln Leu Leu Leu Asn Arg Ile Arg Thr

355	360	365
Trp Gln Lys Thr His Gln Gly Glu Asn Asn Gly Leu Ala Asn Ser Ile 370 375 380		
Arg Asp Ser Leu Asn Glu Tyr Glu Ala Lys Leu Ser Asp Leu Arg Ala 385 390 395 400		
Arg Leu Gln Glu Ala Ala Ala Gln Ala Lys Gln Ala Asn Gly Leu Asn 405 410 415		
Gln Glu Asn Glu Arg Ala Leu Gly Ala Ile Gln Arg Gln Val Lys Glu 420 425 430		
Ile Asn Ser Leu Gln Ser Asp Phe Thr Lys Tyr Leu Thr Thr Ala Asp 435 440 445		
Ser Ser Leu Leu Gln Thr Asn Ile Ala Leu Gln Leu Met Glu Lys Ser 450 455 460		
Gln Lys Glu Tyr Glu Lys Leu Ala Ala Ser Leu Asn Glu Ala Arg Gln 465 470 475 480		
Glu Leu Ser Asp Lys Val Arg Glu Leu Ser Arg Ser Ala Gly Lys Thr 485 490 495		
Ser Leu Val Glu Glu Ala Glu Lys His Ala Arg Ser Leu Gln Glu Leu 500 505 510		
Ala Lys Gln Leu Glu Glu Ile Lys Arg Asn Ala Ser Gly Asp Glu Leu 515 520 525		
Val Arg Cys Ala Val Asp Ala Ala Thr Ala Tyr Glu Asn Ile Leu Asn 530 535 540		
Ala Ile Lys Ala Ala Glu Asp Ala Ala Asn Arg Ala Ala Ser Ala Ser 545 550 555 560		
Glu Ser Ala Leu Gln Thr Val Ile Lys Glu Asp Leu Pro Arg Lys Ala 565 570 575		
Lys Thr Leu Ser Ser Asn Ser Asp Lys Leu Leu Asn Glu Ala Lys Met 580 585 590		
Thr Gln Lys Lys Leu Lys Gln Glu Val Ser Pro Ala Leu Asn Asn Leu 595 600 605		
Gln Gln Thr Leu Asn Ile Val Thr Val Gln Lys Glu Val Ile Asp Thr 610 615 620		
Asn Leu Thr Thr Leu Arg Asp Gly Leu His Gly Ile Gln Arg Gly Asp 625 630 635 640		
Ile Asp Ala Met Ile Ser Ser Ala Lys Ser Met Val Arg Lys Ala Asn 645 650 655		
Asp Ile Thr Asp Glu Val Leu Asp Gly Leu Asn Pro Ile Gln Thr Asp 660 665 670		
Val Glu Arg Ile Lys Asp Thr Tyr Gly Arg Thr Gln Asn Glu Asp Phe 675 680 685		

Lys Lys Ala Leu Thr Asp Ala Asp Asn Ser Val Asn Lys Leu Thr Asn
690 695 700

Lys Leu Pro Asp Leu Trp Arg Lys Ile Glu Ser Ile Asn Gln Gln Leu
705 710 715 720

Leu Pro Leu Gly Asn Ile Ser Asp Asn Met Asp Arg Ile Arg Glu Leu
725 730 735

Ile Gln Gln Ala Arg Asp Ala Ala Ser Lys Val Ala Val Pro Met Arg
740 745 750

Phe Asn Gly Lys Ser Gly Val Glu Val Arg Leu Pro Asn Asp Leu Glu
755 760 765

Asp Leu Lys Gly Tyr Thr Ser Leu Ser Leu Phe Leu Gln Arg Pro Asn
770 775 780

Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr Leu Gly
785 790 795 800

Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val Asp Gly
805 810 815

Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu Leu Gln
820 825 830

Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val Met Asp
835 840 845

Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn Tyr Thr
850 855 860

Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr Asp Met
865 870 875 880

Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu Asn Val
885 890 895

Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro Ser Arg
900 905 910

Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp Leu Asn
915 920 925

Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn Leu Asn
930 935 940

Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser Asp Lys
945 950 955 960

Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln Pro His
965 970 975

Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val Asp Arg
980 985 990

Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Il Ser Leu Asn
995 1000 1005

Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser Glu Leu
1010 1015 1020

Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg Asp His
1025 1030 1035 1040

Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp-Ile Asn
1045 1050 1055

Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp Phe Ser
1060 1065 1070

Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg Phe Asn
1075 1080 1085

Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys Lys Thr
1090 1095 1100

Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys Lys Cys
1105 1110 1115 1120

Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg Gly Gly
1125 1130 1135

Gln Leu Ser Phe Thr Asp Leu Gly Leu Pro Pro Thr Asp His Leu Gln
1140 1145 1150

Ala Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly Ile Leu Leu Asp
1155 1160 1165

His Gln Thr Trp Thr Arg Asn Leu Gln Val Thr Leu Glu Asp Gly Tyr
1170 1175 1180

Ile Glu Leu Ser Thr Ser Asp Ser Gly Gly Pro Ile Phe Lys Ser Pro
1185 1190 1195 1200

Gln Thr Tyr Met Asp Gly Leu Leu His Tyr Val Ser Val Ile Ser Asp
1205 1210 1215

Asn Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Leu Leu Arg Asn Ser
1220 1225 1230

Lys Arg Leu Lys His Ile Ser Ser Ser Arg Gln Ser Leu Arg Leu Gly
1235 1240 1245

Gly Ser Asn Phe Glu Gly Cys Ile Ser Asn Val Phe Val Gln Arg Leu
1250 1255 1260

Ser Leu Ser Pro Glu Val Leu Asp Leu Thr Ser Asn Ser Leu Lys Arg
1265 1270 1275 1280

Asp Val Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe Leu Met
1285 1290 1295

Leu Leu Lys Gly Ser Thr Arg Phe Asn Lys Thr Lys Thr Phe Arg Ile
1300 1305 1310

Asn Gln Leu Leu Gln Asp Thr Pro Val Ala Ser Pro Arg Ser Val Lys
1315 1320 1325

Val Trp Gln Asp Ala Cys Ser Pro Leu Pro Lys Thr Gln Ala Asn His

1330	1335	1340
Gly Ala Leu Gln Phe Gly Asp Ile Pro Thr Ser His Leu Leu Phe Lys		
1345	1350	1355 1360
Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser Gln Phe Ala Val Asp Met		
	1365	1370 1375
Gln Thr Thr Ser Ser Arg Gly Leu Val Phe His Thr Gly Thr Lys Asn		
	1380	1385 1390
Ser Phe Met Ala Leu Tyr Leu Ser Lys Gly Arg Leu Val Phe Ala Leu		
	1395	1400 1405
Gly Thr Asp Gly Lys Lys Leu Arg Ile Lys Ser Lys Glu Lys Cys Asn		
	1410	1415 1420
Asp Gly Lys Trp His Thr Val Val Phe Gly His Asp Gly Glu Lys Gly		
	1425	1430 1435 1440
Arg Leu Val Val Asp Gly Leu Arg Ala Arg Glu Gly Ser Leu Pro Gly		
	1445	1450 1455
Asn Ser Thr Ile Ser Ile Arg Ala Pro Val Tyr Leu Gly Ser Pro Pro		
	1460	1465 1470
Ser Gly Lys Pro Lys Ser Leu Pro Thr Asn Ser Phe Val Gly Cys Leu		
	1475	1480 1485
Lys Asn Phe Gln Leu Asp Ser Lys Pro Leu Tyr Thr Pro Ser Ser Ser		
	1490	1495 1500
Phe Gly Val Ser Ser Cys Leu Gly Gly Pro Leu Glu Lys Gly Ile Tyr		
	1505	1510 1515 1520
Phe Ser Glu Glu Gly Gly His Val Val Leu Ala His Ser Val Leu Leu		
	1525	1530 1535
Gly Pro Glu Phe Lys Leu Val Phe Ser Ile Arg Pro Arg Ser Leu Thr		
	1540	1545 1550
Gly Ile Leu Ile His Ile Gly Ser Gln Pro Gly Lys His Leu Cys Val		
	1555	1560 1565
Tyr Leu Glu Ala Gly Lys Val Thr Ala Ser Met Asp Ser Gly Ala Gly		
	1570	1575 1580
Gly Thr Ser Thr Ser Val Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln		
	1585	1590 1595 1600
Trp His Ser Val Ala Val Thr Ile Lys Gln His Ile Leu His Leu Glu		
	1605	1610 1615
Leu Asp Thr Asp Ser Ser Tyr Thr Ala Gly Gln Ile Pro Phe Pro Pro		
	1620	1625 1630
Ala Ser Thr Gln Glu Pro Leu His Leu Gly Gly Ala Pro Ala Asn Leu		
	1635	1640 1645
Thr Thr Leu Arg Ile Pro Val Trp Lys Ser Phe Phe Gly Cys Leu Arg		
	1650	1655 1660

Asn Ile His Val Asn His Ile Pro Val Pro Val Thr Glu Ala Leu Glu
 1665 1670 1675 1680

Val Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp Gln
 1685 1690

<210> 9
 <211> 5264
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (59)..(5233)

<220>
 <221> sig_peptide
 <222> (59)..(151)

<400> 9
 gtataagagg aagaacacaa aggtttgcag cagccaggca gaacaccaag ggatcaag 58

 atg ccg cct aca gtg agg tgg tca gcc tgg tgc aca gga tgg ctg tgg 106
 Met Pro Pro Thr Val Arg Trp Ser Ala Trp Cys Thr Gly Trp Leu Trp
 1 5 10 15

 atc ttt ggg gca gct ctg ggc cag tgc ctg ggg tat ggc tca gag cag 154
 Ile Phe Gly Ala Ala Leu Gly Gln Cys Leu Gly Tyr Gly Ser Glu Gln
 20 25 30

 caa agg gta gca ttt ctt cag cat cca ggg caa aac cat ctg caa gca 202
 Gln Arg Val Ala Phe Leu Gln His Pro Gly Gln Asn His Leu Gln Ala
 35 40 45

 agt tat atg gag ctt aga ccc agc cag ggc tgt cgc cca gga tac tat 250
 Ser Tyr Met Glu Leu Arg Pro Ser Gln Gly Cys Arg Pro Gly Tyr Tyr
 50 55 60

 cga gac atc aaa agc ttc cct gcg gga agg tct gtt ccc tgc aat tgc 298
 Arg Asp Ile Lys Ser Phe Pro Ala Gly Arg Ser Val Pro Cys Asn Cys
 65 70 75 80

 aac gga cat tca aat aga tgc caa gac ggc tcg gga gtg tgc att aac 346
 Asn Gly His Ser Asn Arg Cys Gln Asp Gly Ser Gly Val Cys Ile Asn
 85 90 95

 tgt cag cac aac aca gct ggg gag cac tgt gag cgt tgc aag agg ggt 394
 Cys Gln His Asn Thr Ala Gly Glu His Cys Glu Arg Cys Lys Arg Gly
 100 105 110

 tac tat gga agc gcc atc cat gga tcc tgc agg gtt tgc ccc tgt cct 442
 Tyr Tyr Gly Ser Ala Ile His Gly Ser Cys Arg Val Cys Pro Cys Pro
 115 120 125

 cac acc aac agc ttt gcc act ggc tgt gct gtg gat gga gga gct gtg 490
 His Thr Asn Ser Phe Ala Thr Gly Cys Ala Val Asp Gly Gly Ala Val
 130 135 140

 agg tgt gcc tgc aaa ccc gga tac aca gga gca cag tgt gag agg tgt 538

Arg Cys Ala Cys Lys Pro Gly Tyr Thr Gly Ala Gln Cys Glu Arg Cys	
145 150 155 160	
gca cca gga tat ttt ggg aac ccc cag aaa ttt gga ggt agc tgc caa	586
Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe Gly Gly Ser Cys Gln	
165 170 175	
cca tgc aat tgc aac agt aat ggc cag ttt ggc act tgt gat ccc cta	634
Pro Cys Asn Cys Asn Ser Asn Gly Gln Phe Gly Thr Cys Asp Pro Leu	
180 185 190	
act gga gac tgt gta agc caa gaa ccc aaa gat ggc agc cct gca gaa	682
Thr Gly Asp Cys Val Ser Gln Glu Pro Lys Asp Gly Ser Pro Ala Glu	
195 200 205	
gaa tgt gat gac tgt gac agc tgt gtg atg act ctc cta aat gac ttg	730
Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr Leu Leu Asn Asp Leu	
210 215 220	
gtc ccc atg ggt gag gaa ctc gcc ctg gtg aaa tca aaa ctt cag ggg	778
Val Pro Met Gly Glu Leu Ala Leu Val Lys Ser Lys Leu Gln Gly	
225 230 235 240	
ctg agt gtg aac act ggt tct ctg gaa cag atc cgg cat gtg gag atg	826
Leu Ser Val Asn Thr Gly Ser Leu Glu Gln Ile Arg His Val Glu Met	
245 250 255	
cag gcc aag gac ctg agg aac cag ctg ctt ggc ttc cgt tcc gcc atc	874
Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Gly Phe Arg Ser Ala Ile	
260 265 270	
tcc agt cac ggg tcc caa atg gac ggc ctg gaa aaa gaa ctc agt cat	922
Ser Ser His Gly Ser Gln Met Asp Gly Leu Glu Lys Glu Leu Ser His	
275 280 285	
ttg tac cag gaa ttc gaa act ttg caa gaa aag gcg cag gtc aat tcc	970
Leu Tyr Gln Glu Phe Glu Thr Leu Gln Glu Lys Ala Gln Val Asn Ser	
290 295 300	
aga aaa gca caa aca tta tat aac aac atc gat acg aca atc caa aac	1018
Arg Lys Ala Gln Thr Leu Tyr Asn Asn Ile Asp Thr Thr Ile Gln Asn	
305 310 315 320	
gcc aaa gag ttg gac atg aag att aaa aac ata ctt acg aat gtg cac	1066
Ala Lys Glu Leu Asp Met Lys Ile Lys Asn Ile Leu Thr Asn Val His	
325 330 335	
att ctc ctg aag cag atc gct cgg cca ggt gga gaa gga atg gac ttg	1114
Ile Leu Leu Lys Gln Ile Ala Arg Pro Gly Gly Glu Gly Met Asp Leu	
340 345 350	
ccg gtg ggc gac tgg tcc agg gag tcg gcg gaa gct cag cgc atg ttg	1162
Pro Val Gly Asp Trp Ser Arg Glu Ser Ala Glu Ala Gln Arg Met Leu	
355 360 365	
cgg gag ctg cga ggc cga gac ttt aaa aag cac ctc caa gaa gca gag	1210
Arg Glu Leu Arg Gly Arg Asp Phe Lys Lys His Leu Gln Glu Ala Glu	
370 375 380	
gcc cag aaa atg gaa gcc cag ctc tta ctg aac cga atc agg acc tgg	1258
Ala Gln Lys Met Glu Ala Gln Leu Leu Leu Asn Arg Ile Arg Thr Trp	

385	390	395	400	
ctg gaa tcc cac cag gtg gag aac aat gga ctg cta aag aat att cgg				1306
Leu Glu Ser His Gln Val Glu Asn Asn Gly Leu Leu Lys Asn Ile Arg				
	405	410	415	
gat tca tta aat gat tat gaa gcc aaa ctt cag gac ctg cgt tcc gtg				1354
Asp Ser Leu Asn Asp Tyr Glu Ala Lys Leu Gln Asp Leu Arg Ser Val				
	420	425	430	
ctt cag gag gcg gca gcc cag gga aag cag gct aca ggc ctc aac cac				1402
Leu Gln Glu Ala Ala Ala Gln Gly Lys Gln Ala Thr Gly Leu Asn His				
	435	440	445	
gaa aat gag ggg gtc cta gga gcc atc cag aga caa atg aag gaa atg				1450
Glu Asn Glu Gly Val Leu Gly Ala Ile Gln Arg Gln Met Lys Glu Met				
	450	455	460	
gat tcc ctg aag aag tac ctc acc gag cac ctg gcc aca gca gac gct				1498
Asp Ser Leu Lys Lys Tyr Leu Thr Glu His Leu Ala Thr Ala Asp Ala				
	465	470	475	480
tcc ctg ctg caa acc aac agt cta ctg cag cgg atg gac acg agc cag				1546
Ser Leu Leu Gln Thr Asn Ser Leu Leu Gln Arg Met Asp Thr Ser Gln				
	485	490	495	
aag gag tat gaa agc tta gct gct gct tta aac gga gca aga cag gaa				1594
Lys Glu Tyr Glu Ser Leu Ala Ala Ala Leu Asn Gly Ala Arg Gln Glu				
	500	505	510	
ctg aat gac caa gtg cgg gaa ctc tcc aga tcc gga ggc aaa gca ccc				1642
Leu Asn Asp Gln Val Arg Glu Leu Ser Arg Ser Gly Gly Lys Ala Pro				
	515	520	525	
ctg gtg gct gag gcc gag aag cac gct cag tct tta cag gag ctg gca				1690
Leu Val Ala Glu Ala Glu Lys His Ala Gln Ser Leu Gln Glu Leu Ala				
	530	535	540	
aag cag ctg gaa gag ata aag aga aac acc agt ggg gat gag tcg gtg				1738
Lys Gln Leu Glu Glu Ile Lys Arg Asn Thr Ser Gly Asp Glu Ser Val				
	545	550	555	560
cgc tgt gtc gtg gac gct gcc act gcc tat gag agc atc ctc aac gcc				1786
Arg Cys Val Val Asp Ala Ala Thr Ala Tyr Glu Ser Ile Leu Asn Ala				
	565	570	575	
atc cga gca gca gag gat gca gcc ggc aag gcc gac agt gcc tca gag				1834
Ile Arg Ala Ala Glu Asp Ala Ala Gly Lys Ala Asp Ser Ala Ser Glu				
	580	585	590	
tcc gcc ttc cag aca gtg ata aag gaa gat ctt ccg aga aga gcc aaa				1882
Ser Ala Phe Gln Thr Val Ile Lys Glu Asp Leu Pro Arg Arg Ala Lys				
	595	600	605	
acc ctg agt tct gac agc gag gaa ctg tta aac gag gcc aag atg aca				1930
Thr Leu Ser Ser Asp Ser Glu Glu Leu Leu Asn Glu Ala Lys Met Thr				
	610	615	620	
cgg aaa agg cta cag caa gaa atc aat cca gct ctc aac agc cta cag				1978
Arg Lys Arg Leu Gln Gln Glu Ile Asn Pro Ala Leu Asn Ser Leu Gln				
	625	630	635	640

caa acc ctg aag act gta tca gtt cag aag gac ctg cta gat gcc aat	2026
Gln Thr Leu Lys Thr Val Ser Val Gln Lys Asp Leu Leu Asp Ala Asn	
645 650 655	
gtc act gct gtc cgt aat gac ctt cgt ggg atc cag aga ggt gat att	2074
Val Thr Ala Val Arg Asn Asp Leu Arg Gly Ile Gln Arg Gly Asp Ile	
660 665 670	
gac agt gtg gtg agt gga gcg aag agc atg gtc agg aaa gcc aat ggg	2122
Asp Ser Val Val Ser Gly Ala Lys Ser Met Val Arg Lys Ala Asn Gly	
675 680 685	
ata acg agc gag gtc ctg gac ggg ctc agc ccc atc cag acg gat ttg	2170
Ile Thr Ser Glu Val Leu Asp Gly Leu Ser Pro Ile Gln Thr Asp Leu	
690 695 700	
gga agg att aag gac agc tac ggg agc aca cgg cat gag gac ttc aac	2218
Gly Arg Ile Lys Asp Ser Tyr Gly Ser Thr Arg His Glu Asp Phe Asn	
705 710 715 720	
aaa gct ctg att gac gcc aat aac tca gta aag aaa tta acc aag aag	2266
Lys Ala Leu Ile Asp Ala Asn Asn Ser Val Lys Lys Leu Thr Lys Lys	
725 730 735	
ttg cct gat ctt ttt gtc aag att gaa agc atc aat caa cag ttg ctg	2314
Leu Pro Asp Leu Phe Val Lys Ile Glu Ser Ile Asn Gln Gln Leu Leu	
740 745 750	
ccc ctg gga aac atc tct gac aat gta gac cga atc cga gag ctc att	2362
Pro Leu Gly Asn Ile Ser Asp Asn Val Asp Arg Ile Arg Glu Leu Ile	
755 760 765	
acg cag gcc aga gat gct gcg aac aag gtt gca att ccc atg agg ttc	2410
Thr Gln Ala Arg Asp Ala Ala Asn Lys Val Ala Ile Pro Met Arg Phe	
770 775 780	
aat ggt aaa tct ggt gtt gaa gtc cgt ctg cca aat gac cta gaa gac	2458
Asn Gly Lys Ser Gly Val Glu Val Arg Leu Pro Asn Asp Leu Glu Asp	
785 790 795 800	
ttg aag gga tac acg tct ctg tct ttg ttc ctc caa aga cca gac tta	2506
Leu Lys Gly Tyr Thr Ser Leu Ser Leu Phe Leu Gln Arg Pro Asp Leu	
805 810 815	
aga gag aat gga ggc act gag gac atg ttt gta atg tac ctt gga aac	2554
Arg Glu Asn Gly Gly Thr Glu Asp Met Phe Val Met Tyr Leu Gly Asn	
820 825 830	
aag gat gcc tcc aag gac tac atc ggc atg gcg gtt gta gat ggc cag	2602
Lys Asp Ala Ser Lys Asp Tyr Ile Gly Met Ala Val Val Asp Gly Gln	
835 840 845	
ctg acg tgt gtc tac aac ctg ggg gac cga gaa gct gaa gtt cag atc	2650
Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu Val Gln Ile	
850 855 860	
gat cag gtc ctg acg gag agt gag tct cag gag gca gtt atg gac cgg	2698
Asp Gln Val Leu Thr Glu Ser Glu Ser Gln Glu Ala Val Met Asp Arg	
865 870 875 880	

gtg aag ttc cag aga ata tat caa ttt gcc aag ctt aat tac acc aaa	2746
Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Lys Leu Asn Tyr Thr Lys	
885 890 895	
gaa gcc acg tcc aat aaa ccc aaa gct ccc gcg gtc tac gac ctg gag	2794
Glu Ala Thr Ser Asn Lys Pro Lys Ala Pro Ala Val Tyr Asp Leu Glu	
900 905 910	
ggt ggc agt agc aac acg ctc ctt aat ttg gat ccc gag gac gct gtg	2842
Gly Gly Ser Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu Asp Ala Val	
915 920 925	
ttt tat gtc gga ggt tac cca ccg gat ttt gaa ctt cct agc aga ctg	2890
Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Glu Leu Pro Ser Arg Leu	
930 935 940	
cgg ttc cct cca tac aaa ggc tgt atc gaa cta gat gac ctc aat gaa	2938
Arg Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp Leu Asn Glu	
945 950 955 960	
aac gtt cta agc ttg tac aat ttc aag aca act ttc aat ctc aac acc	2986
Asn Val Leu Ser Leu Tyr Asn Phe Lys Thr Thr Phe Asn Leu Asn Thr	
965 970 975	
acg gag gtg gag cct tgt agg agg aga aag gaa gag tca gac aaa aat	3034
Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser Asp Lys Asn	
980 985 990	
tac ttt gaa ggt aca ggc tat gct cgc atc cct act caa cca aat gct	3082
Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Ile Pro Thr Gln Pro Asn Ala	
995 1000 1005	
ccc ttc cca aac ttc ata cag acc atc cag act act gtg gac aga ggt	3130
Pro Phe Pro Asn Phe Ile Gln Thr Ile Gln Thr Thr Val Asp Arg Gly	
1010 1015 1020	
tta ctg ttc ttc gca gaa aac cag gat aac ttc ata tct ctg aac ata	3178
Leu Leu Phe Phe Ala Glu Asn Gln Asp Asn Phe Ile Ser Leu Asn Ile	
1025 1030 1035 1040	
gaa gat ggc aat ctc atg gtg aga tac aaa cta aat tca gag cca ccc	3226
Glu Asp Gly Asn Leu Met Val Arg Tyr Lys Leu Asn Ser Glu Pro Pro	
1045 1050 1055	
aaa gag aag gga att cga gac acc atc aac gat ggg aaa gat cat tcg	3274
Lys Glu Lys Gly Ile Arg Asp Thr Ile Asn Asp Gly Lys Asp His Ser	
1060 1065 1070	
atc tta atc aca att gga aaa cta caa aaa cgc atg tgg ata aat gtg	3322
Ile Leu Ile Thr Ile Gly Lys Leu Gln Lys Arg Met Trp Ile Asn Val	
1075 1080 1085	
aac gaa cgc agt gta cga atc gaa ggg gaa ata ttt gat ttc agc aca	3370
Asn Glu Arg Ser Val Arg Ile Glu Gly Glu Ile Phe Asp Phe Ser Thr	
1090 1095 1100	
tat tat ttg ggc gga att cca att gca atc aga gaa agg ttt aac atc	3418
Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg Phe Asn Ile	
1105 1110 1115 1120	
tca acg cct gct ttc caa ggc tgc atg aag aat ctg aag aaa acc agt	3466

Ser Thr Pro Ala Phe Gln Gly Cys Met Lys Asn Leu Lys Lys Thr Ser	
1125 1130 1135	
ggg gtt gtc agg ttg aat gat act gtg ggt gta acc aag aag tgc tca	3514
Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys Lys Cys Ser	
1140 1145 1150	
gaa gac tgg aag ctt gtg cga acc gcc tcg ttc tcc aga gga ggg cag	3562
Glu Asp Trp Lys Leu Val Arg Thr Ala Ser Phe Ser Arg Gly Gly Gln	
1155 1160 1165	
atg agc ttt aca aac ttg gac gtg ccc tcg act gac cgc ttc cag ctc	3610
Met Ser Phe Thr Asn Leu Asp Val Pro Ser Thr Asp Arg Phe Gln Leu	
1170 1175 1180	
tcc ttt ggg ttt cag acc ttt caa ccc agt ggc aca ctg ctc aat cat	3658
Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly Thr Leu Leu Asn His	
1185 1190 1195 1200	
cag acg cgg aca agc agc ctg ctg gtc acc ctg gaa gat ggg cac att	3706
Gln Thr Arg Thr Ser Ser Leu Leu Val Thr Leu Glu Asp Gly His Ile	
1205 1210 1215	
gag ttg agc act agg gac agc aac atc cca att ttc aag tct cca ggg	3754
Glu Leu Ser Thr Arg Asp Ser Asn Ile Pro Ile Phe Lys Ser Pro Gly	
1220 1225 1230	
acc tac atg gac ggt tta ctg cat cat gta tct gta ata agt gac acc	3802
Thr Tyr Met Asp Gly Leu Leu His His Val Ser Val Ile Ser Asp Thr	
1235 1240 1245	
tca ggt ctc cgc ctt ctc atc gat gac cag gtc ctg aga agg aac cag	3850
Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Val Leu Arg Arg Asn Gln	
1250 1255 1260	
agg ctt cct agc ttc tct aac gcc cag cag tcg ctc cgc ctt gga gga	3898
Arg Leu Pro Ser Phe Ser Asn Ala Gln Gln Ser Leu Arg Leu Gly Gly	
1265 1270 1275 1280	
ggt cat ttc gag ggt tgt atc agc aat gtt tta gtc caa agg ttt tca	3946
Gly His Phe Glu Gly Cys Ile Ser Asn Val Leu Val Gln Arg Phe Ser	
1285 1290 1295	
cag agt cca gaa gtc ctg gat ctg gcc agt aaa tct acc aag aag gat	3994
Gln Ser Pro Glu Val Leu Asp Leu Ala Ser Lys Ser Thr Lys Lys Asp	
1300 1305 1310	
gca tcc cta gga ggc tgc agt tta aac aag cca cct ttt ctt atg ttg	4042
Ala Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe Leu Met Leu	
1315 1320 1325	
ttt aaa agt ccc aag aga ttt aac aag ggc cgg att ttc aat gtt aat	4090
Phe Lys Ser Pro Lys Arg Phe Asn Lys Gly Arg Ile Phe Asn Val Asn	
1330 1335 1340	
cag ctg atg caa gat gca cct cag gcc aca agg agc aca gag gct tgg	4138
Gln Leu Met Gln Asp Ala Pro Gln Ala Thr Arg Ser Thr Glu Ala Trp	
1345 1350 1355 1360	
caa gat ggg agg tcc tgc cta cca cct ctg aac acc aag gcc tct cac	4186
Gln Asp Gly Arg Ser Cys Leu Pro Pro Leu Asn Thr Lys Ala Ser His	

1365	1370	1375	
aga gcc ctg cag ttt gga gac agc ccc acc agc cac ttg cta ctc aag			4234
Arg Ala Leu Gln Phe Gly Asp Ser Pro Thr Ser His Leu Leu Leu Lys			
1380	1385	1390	
ctt ccc cag gaa ctg ctg aaa cct agg tca cag ttt tct tta gac ata			4282
Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser Gln Phe Ser Leu Asp Ile			
1395	1400	1405	
cag aca act tcc ccc aaa gga ctg gtg ttt tac gca ggc acc aag gac			4330
Gln Thr Thr Ser Pro Lys Gly Leu Val Phe Tyr Ala Gly Thr Lys Asp			
1410	1415	1420	
tcc ttc ctg gct ctt tat gtc gca gat ggc cgt gtt gtc ttt gct ttg			4378
Ser Phe Leu Ala Leu Tyr Val Ala Asp Gly Arg Val Val Phe Ala Leu			
1425	1430	1435	1440
ggg gca gga ggg aag aaa ctg aga ctc agg agc aag gag aga tac cat			4426
Gly Ala Gly Gly Lys Lys Leu Arg Leu Arg Ser Lys Glu Arg Tyr His			
1445	1450	1455	
gac ggg aag tgg cac acg gtg gtg ttc gga cta aat gga gga aag gca			4474
Asp Gly Lys Trp His Thr Val Val Phe Gly Leu Asn Gly Gly Lys Ala			
1460	1465	1470	
cgc ctg gtt gtg gat ggg cta agg gcc cag gaa ggc agt ttg cct gga			4522
Arg Leu Val Val Asp Gly Leu Arg Ala Gln Glu Gly Ser Leu Pro Gly			
1475	1480	1485	
aat tct acc atc agc ccc aga gaa cag gtt tac cta ggg ttg ccg cta			4570
Asn Ser Thr Ile Ser Pro Arg Glu Gln Val Tyr Leu Gly Leu Pro Leu			
1490	1495	1500	
tca aga aag cca aag agc cta ccc cag cac agt ttt gtg ggg tgc ctg			4618
Ser Arg Lys Pro Lys Ser Leu Pro Gln His Ser Phe Val Gly Cys Leu			
1505	1510	1515	1520
aga gat ttc cag ttg aac tcg aaa ccc ctg gat tct cct tct gcg agg			4666
Arg Asp Phe Gln Leu Asn Ser Lys Pro Leu Asp Ser Pro Ser Ala Arg			
1525	1530	1535	
ttt ggg gta tct ccc tgc ttg ggt ggc tct tta gag aaa ggc att tat			4714
Phe Gly Val Ser Pro Cys Leu Gly Gly Ser Leu Glu Lys Gly Ile Tyr			
1540	1545	1550	
ttc tcc caa gga gga ggc cat gtg atc cta gcc aat tct gtg tcc ttg			4762
Phe Ser Gln Gly Gly Gly His Val Ile Leu Ala Asn Ser Val Ser Leu			
1555	1560	1565	
ggg cca gag ctt aag ctc act ttc agc att cgc cca cgg agt ctc act			4810
Gly Pro Glu Leu Lys Leu Thr Phe Ser Ile Arg Pro Arg Ser Leu Thr			
1570	1575	1580	
ggg gtc tta ata cac gtc gga agt caa tct gga cag cgc tta agt gtg			4858
Gly Val Leu Ile His Val Gly Ser Gln Ser Gly Gln Arg Leu Ser Val			
1585	1590	1595	1600
tac atg gag gca gga aag gtc aca acc tct gtg agc agt gat gca gga			4906
Tyr Met Glu Ala Gly Lys Val Thr Thr Ser Val Ser Ser Asp Ala Gly			
1605	1610	1615	

gga agt gtg aca tca att aca ccg aag cag tct ctg tgt gat gga cag 4954
 Gly Ser Val Thr Ser Ile Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln
 1620 1625 1630
 tgg cac tcg gtg gca gtc tcc att aaa cag cgc atc ctg cat cta gaa 5002
 Trp His Ser Val Ala Val Ser Ile Lys Gln Arg Ile Leu His Leu Glu
 1635 1640 1645
 ctg gat aca gac agt agc tac aca gtc gca cca ctt tcc ttc tca cca 5050
 Leu Asp Thr Asp Ser Ser Tyr Thr Val Ala Pro Leu Ser Phe Ser Pro
 1650 1655 1660
 aac agc acc cga ggg tca ctg cac gtc gga ggt gtc cca gac aaa ttg 5098
 Asn Ser Thr Arg Gly Ser Leu His Val Gly Gly Val Pro Asp Lys Leu
 1665 1670 1675 1680
 aaa atg ctt aca ctc cct gtg tgg aac tca ttt ttt ggc tgt ctg aag 5146
 Lys Met Leu Thr Leu Pro Val Trp Asn Ser Phe Phe Gly Cys Leu Lys
 1685 1690 1695
 aat att caa gtc aac cat gtc cct gtc ccc atc aca gaa gcc aca gaa 5194
 Asn Ile Gln Val Asn His Val Pro Val Pro Ile Thr Glu Ala Thr Glu
 1700 1705 1710
 gtc caa ggt tct gtc agc ctg aat ggc tgc cct gac cac taaccctaca 5243
 Val Gln Gly Ser Val Ser Leu Asn Gly Cys Pro Asp His
 1715 1720 1725
 cagcaagatt cacctttgga g 5264

<210> 10
 <211> 1725
 <212> PRT
 <213> Rattus norvegicus

<400> 10
 Met Pro Pro Thr Val Arg Trp Ser Ala Trp Cys Thr Gly Trp Leu Trp
 1 5 10 15
 Ile Phe Gly Ala Ala Leu Gly Gln Cys Leu Gly Tyr Gly Ser Glu Gln
 20 25 30
 Gln Arg Val Ala Phe Leu Gln His Pro Gly Gln Asn His Leu Gln Ala
 35 40 45
 Ser Tyr Met Glu Leu Arg Pro Ser Gln Gly Cys Arg Pro Gly Tyr Tyr
 50 55 60
 Arg Asp Ile Lys Ser Phe Pro Ala Gly Arg Ser Val Pro Cys Asn Cys
 65 70 75 80
 Asn Gly His Ser Asn Arg Cys Gln Asp Gly Ser Gly Val Cys Ile Asn
 85 90 95
 Cys Gln His Asn Thr Ala Gly Glu His Cys Glu Arg Cys Lys Arg Gly
 100 105 110
 Tyr Tyr Gly Ser Ala Ile His Gly Ser Cys Arg Val Cys Pro Cys Pro
 115 120 125

His Thr Asn Ser Phe Ala Thr Gly Cys Ala Val Asp Gly Gly Ala Val
 130 135 140
 Arg Cys Ala Cys Lys Pro Gly Tyr Thr Gly Ala Gln Cys Glu Arg Cys
 145 150 155 160
 Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe Gly Gly Ser Cys Gln
 165 170 175
 Pro Cys Asn Cys Asn Ser Asn Gly Gln Phe Gly Thr Cys Asp Pro Leu
 180 185 190
 Thr Gly Asp Cys Val Ser Gln Glu Pro Lys Asp Gly Ser Pro Ala Glu
 195 200 205
 Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr Leu Leu Asn Asp Leu
 210 215 220
 Val Pro Met Gly Glu Glu Leu Ala Leu Val Lys Ser Lys Leu Gln Gly
 225 230 235 240
 Leu Ser Val Asn Thr Gly Ser Leu Glu Gln Ile Arg His Val Glu Met
 245 250 255
 Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Gly Phe Arg Ser Ala Ile
 260 265 270
 Ser Ser His Gly Ser Gln Met Asp Gly Leu Glu Lys Glu Leu Ser His
 275 280 285
 Leu Tyr Gln Glu Phe Glu Thr Leu Gln Glu Lys Ala Gln Val Asn Ser
 290 295 300
 Arg Lys Ala Gln Thr Leu Tyr Asn Asn Ile Asp Thr Thr Ile Gln Asn
 305 310 315 320
 Ala Lys Glu Leu Asp Met Lys Ile Lys Asn Ile Leu Thr Asn Val His
 325 330 335
 Ile Leu Leu Lys Gln Ile Ala Arg Pro Gly Gly Glu Gly Met Asp Leu
 340 345 350
 Pro Val Gly Asp Trp Ser Arg Glu Ser Ala Glu Ala Gln Arg Met Leu
 355 360 365
 Arg Glu Leu Arg Gly Arg Asp Phe Lys Lys His Leu Gln Glu Ala Glu
 370 375 380
 Ala Gln Lys Met Glu Ala Gln Leu Leu Leu Asn Arg Ile Arg Thr Trp
 385 390 395 400
 Leu Glu Ser His Gln Val Glu Asn Asn Gly Leu Leu Lys Asn Ile Arg
 405 410 415
 Asp Ser Leu Asn Asp Tyr Glu Ala Lys Leu Gln Asp Leu Arg Ser Val
 420 425 430
 Leu Gln Glu Ala Ala Ala Gln Gly Lys Gln Ala Thr Gly Leu Asn His
 435 440 445

Glu Asn Glu Gly Val Leu Gly Ala Ile Gln Arg Gln Met Lys Glu Met
450 455 460

Asp Ser Leu Lys Lys Tyr Leu Thr Glu His Leu Ala Thr Ala Asp Ala
465 470 475 480

Ser Leu Leu Gln Thr Asn Ser Leu Leu Gln Arg Met Asp Thr Ser Gln
485 490 495

Lys Glu Tyr Glu Ser Leu Ala Ala Ala Leu Asn Gly Ala Arg Gln Glu
500 505 510

Leu Asn Asp Gln Val Arg Glu Leu Ser Arg Ser Gly Gly Lys Ala Pro
515 520 525

Leu Val Ala Glu Ala Glu Lys His Ala Gln Ser Leu Gln Glu Leu Ala
530 535 540

Lys Gln Leu Glu Glu Ile Lys Arg Asn Thr Ser Gly Asp Glu Ser Val
545 550 555 560

Arg Cys Val Val Asp Ala Ala Thr Ala Tyr Glu Ser Ile Leu Asn Ala
565 570 575

Ile Arg Ala Ala Glu Asp Ala Ala Gly Lys Ala Asp Ser Ala Ser Glu
580 585 590

Ser Ala Phe Gln Thr Val Ile Lys Glu Asp Leu Pro Arg Arg Ala Lys
595 600 605

Thr Leu Ser Ser Asp Ser Glu Glu Leu Leu Asn Glu Ala Lys Met Thr
610 615 620

Arg Lys Arg Leu Gln Gln Glu Ile Asn Pro Ala Leu Asn Ser Leu Gln
625 630 635 640

Gln Thr Leu Lys Thr Val Ser Val Gln Lys Asp Leu Leu Asp Ala Asn
645 650 655

Val Thr Ala Val Arg Asn Asp Leu Arg Gly Ile Gln Arg Gly Asp Ile
660 665 670

Asp Ser Val Val Ser Gly Ala Lys Ser Met Val Arg Lys Ala Asn Gly
675 680 685

Ile Thr Ser Glu Val Leu Asp Gly Leu Ser Pro Ile Gln Thr Asp Leu
690 695 700

Gly Arg Ile Lys Asp Ser Tyr Gly Ser Thr Arg His Glu Asp Phe Asn
705 710 715 720

Lys Ala Leu Ile Asp Ala Asn Asn Ser Val Lys Lys Leu Thr Lys Lys
725 730 735

Leu Pro Asp Leu Phe Val Lys Ile Glu Ser Ile Asn Gln Gln Leu Leu
740 745 750

Pro Leu Gly Asn Ile Ser Asp Asn Val Asp Arg Ile Arg Glu Leu Ile
755 760 765

Thr Gln Ala Arg Asp Ala Ala Asn Lys Val Ala Ile Pro Met Arg Phe

770					775					780					
Asn	Gly	Lys	Ser	Gly	Val	Glu	Val	Arg	Leu	Pro	Asn	Asp	Leu	Glu	Asp
785					790					795					800
Leu	Lys	Gly	Tyr	Thr	Ser	Leu	Ser	Leu	Phe	Leu	Gln	Arg	Pro	Asp	Leu
				805					810					815	
Arg	Glu	Asn	Gly	Gly	Thr	Glu	Asp	Met	Phe	Val	Met	Tyr	Leu	Gly	Asn
			820					825					830		
Lys	Asp	Ala	Ser	Lys	Asp	Tyr	Ile	Gly	Met	Ala	Val	Val	Asp	Gly	Gln
		835					840					845			
Leu	Thr	Cys	Val	Tyr	Asn	Leu	Gly	Asp	Arg	Glu	Ala	Glu	Val	Gln	Ile
	850					855					860				
Asp	Gln	Val	Leu	Thr	Glu	Ser	Glu	Ser	Gln	Glu	Ala	Val	Met	Asp	Arg
865					870					875					880
Val	Lys	Phe	Gln	Arg	Ile	Tyr	Gln	Phe	Ala	Lys	Leu	Asn	Tyr	Thr	Lys
				885					890					895	
Glu	Ala	Thr	Ser	Asn	Lys	Pro	Lys	Ala	Pro	Ala	Val	Tyr	Asp	Leu	Glu
			900					905					910		
Gly	Gly	Ser	Ser	Asn	Thr	Leu	Leu	Asn	Leu	Asp	Pro	Glu	Asp	Ala	Val
		915					920					925			
Phe	Tyr	Val	Gly	Gly	Tyr	Pro	Pro	Asp	Phe	Glu	Leu	Pro	Ser	Arg	Leu
	930					935					940				
Arg	Phe	Pro	Pro	Tyr	Lys	Gly	Cys	Ile	Glu	Leu	Asp	Asp	Leu	Asn	Glu
945					950					955					960
Asn	Val	Leu	Ser	Leu	Tyr	Asn	Phe	Lys	Thr	Thr	Phe	Asn	Leu	Asn	Thr
				965					970					975	
Thr	Glu	Val	Glu	Pro	Cys	Arg	Arg	Arg	Lys	Glu	Glu	Ser	Asp	Lys	Asn
			980					985					990		
Tyr	Phe	Glu	Gly	Thr	Gly	Tyr	Ala	Arg	Ile	Pro	Thr	Gln	Pro	Asn	Ala
		995					1000					1005			
Pro	Phe	Pro	Asn	Phe	Ile	Gln	Thr	Ile	Gln	Thr	Thr	Val	Asp	Arg	Gly
	1010					1015						1020			
Leu	Leu	Phe	Phe	Ala	Glu	Asn	Gln	Asp	Asn	Phe	Ile	Ser	Leu	Asn	Ile
1025				1030						1035					1040
Glu	Asp	Gly	Asn	Leu	Met	Val	Arg	Tyr	Lys	Leu	Asn	Ser	Glu	Pro	Pro
			1045						1050				1055		
Lys	Glu	Lys	Gly	Ile	Arg	Asp	Thr	Ile	Asn	Asp	Gly	Lys	Asp	His	Ser
			1060					1065					1070		
Ile	Leu	Ile	Thr	Ile	Gly	Lys	Leu	Gln	Lys	Arg	Met	Trp	Ile	Asn	Val
			1075				1080					1085			
Asn	Glu	Arg	Ser	Val	Arg	Ile	Glu	Gly	Glu	Ile	Phe	Asp	Phe	Ser	Thr
	1090					1095					1100				

Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg Phe Asn Ile
1105 1110 1115 1120

Ser Thr Pro Ala Phe Gln Gly Cys Met Lys Asn Leu Lys Lys Thr Ser
1125 1130 1135

Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys Lys Cys Ser
1140 1145 1150

Glu Asp Trp Lys Leu Val Arg Thr Ala Ser Phe Ser Arg Gly Gly Gln
1155 1160 1165

Met Ser Phe Thr Asn Leu Asp Val Pro Ser Thr Asp Arg Phe Gln Leu
1170 1175 1180

Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly Thr Leu Leu Asn His
1185 1190 1195 1200

Gln Thr Arg Thr Ser Ser Leu Leu Val Thr Leu Glu Asp Gly His Ile
1205 1210 1215

Glu Leu Ser Thr Arg Asp Ser Asn Ile Pro Ile Phe Lys Ser Pro Gly
1220 1225 1230

Thr Tyr Met Asp Gly Leu Leu His His Val Ser Val Ile Ser Asp Thr
1235 1240 1245

Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Val Leu Arg Arg Asn Gln
1250 1255 1260

Arg Leu Pro Ser Phe Ser Asn Ala Gln Gln Ser Leu Arg Leu Gly Gly
1265 1270 1275 1280

Gly His Phe Glu Gly Cys Ile Ser Asn Val Leu Val Gln Arg Phe Ser
1285 1290 1295

Gln Ser Pro Glu Val Leu Asp Leu Ala Ser Lys Ser Thr Lys Lys Asp
1300 1305 1310

Ala Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe Leu Met Leu
1315 1320 1325

Phe Lys Ser Pro Lys Arg Phe Asn Lys Gly Arg Ile Phe Asn Val Asn
1330 1335 1340

Gln Leu Met Gln Asp Ala Pro Gln Ala Thr Arg Ser Thr Glu Ala Trp
1345 1350 1355 1360

Gln Asp Gly Arg Ser Cys Leu Pro Pro Leu Asn Thr Lys Ala Ser His
1365 1370 1375

Arg Ala Leu Gln Phe Gly Asp Ser Pro Thr Ser His Leu Leu Leu Lys
1380 1385 1390

Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser Gln Phe Ser Leu Asp Ile
1395 1400 1405

Gln Thr Thr Ser Pro Lys Gly Leu Val Phe Tyr Ala Gly Thr Lys Asp
1410 1415 1420

Ser Phe Leu Ala Leu Tyr Val Ala Asp Gly Arg Val Val Phe Ala Leu
1425 1430 1435 1440

Gly Ala Gly Gly Lys Lys Leu Arg Leu Arg Ser Lys Glu Arg Tyr His
1445 1450 1455

Asp Gly Lys Trp His Thr Val Val Phe Gly Leu Asn Gly Gly Lys Ala
1460 1465 1470

Arg Leu Val Val Asp Gly Leu Arg Ala Gln Glu Gly Ser Leu Pro Gly
1475 1480 1485

Asn Ser Thr Ile Ser Pro Arg Glu Gln Val Tyr Leu Gly Leu Pro Leu
1490 1495 1500

Ser Arg Lys Pro Lys Ser Leu Pro Gln His Ser Phe Val Gly Cys Leu
1505 1510 1515 1520

Arg Asp Phe Gln Leu Asn Ser Lys Pro Leu Asp Ser Pro Ser Ala Arg
1525 1530 1535

Phe Gly Val Ser Pro Cys Leu Gly Gly Ser Leu Glu Lys Gly Ile Tyr
1540 1545 1550

Phe Ser Gln Gly Gly Gly His Val Ile Leu Ala Asn Ser Val Ser Leu
1555 1560 1565

Gly Pro Glu Leu Lys Leu Thr Phe Ser Ile Arg Pro Arg Ser Leu Thr
1570 1575 1580

Gly Val Leu Ile His Val Gly Ser Gln Ser Gly Gln Arg Leu Ser Val
1585 1590 1595 1600

Tyr Met Glu Ala Gly Lys Val Thr Thr Ser Val Ser Ser Asp Ala Gly
1605 1610 1615

Gly Ser Val Thr Ser Ile Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln
1620 1625 1630

Trp His Ser Val Ala Val Ser Ile Lys Gln Arg Ile Leu His Leu Glu
1635 1640 1645

Leu Asp Thr Asp Ser Ser Tyr Thr Val Ala Pro Leu Ser Phe Ser Pro
1650 1655 1660

Asn Ser Thr Arg Gly Ser Leu His Val Gly Gly Val Pro Asp Lys Leu
1665 1670 1675 1680

Lys Met Leu Thr Leu Pro Val Trp Asn Ser Phe Phe Gly Cys Leu Lys
1685 1690 1695

Asn Ile Gln Val Asn His Val Pro Val Pro Ile Thr Glu Ala Thr Glu
1700 1705 1710

Val Gln Gly Ser Val Ser Leu Asn Gly Cys Pro Asp His
1715 1720 1725

<210> 11
<211> 5113
<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(5082)

<400> 11

cag	caa	agg	gta	gca	ttt	ctt	cag	cat	cca	ggg	caa	aac	cat	ctg	caa	48
Gln	Gln	Arg	Val	Ala	Phe	Leu	Gln	His	Pro	Gly	Gln	Asn	His	Leu	Gln	
1				5					10					15		
gca	agt	tat	atg	gag	ctt	aga	ccc	agc	cag	ggc	tgt	cgc	cca	gga	tac	96
Ala	Ser	Tyr	Met	Glu	Leu	Arg	Pro	Ser	Gln	Gly	Cys	Arg	Pro	Gly	Tyr	
			20					25					30			
tat	cga	gac	atc	aaa	agc	ttc	cct	gcg	gga	agg	tct	gtt	ccc	tgc	aat	144
Tyr	Arg	Asp	Ile	Lys	Ser	Phe	Pro	Ala	Gly	Arg	Ser	Val	Pro	Cys	Asn	
		35					40					45				
tgc	aac	gga	cat	tca	aat	aga	tgc	caa	gac	ggc	tcg	gga	gtg	tgc	att	192
Cys	Asn	Gly	His	Ser	Asn	Arg	Cys	Gln	Asp	Gly	Ser	Gly	Val	Cys	Ile	
	50					55				60						
aac	tgt	cag	cac	aac	aca	gct	ggg	gag	cac	tgt	gag	cgt	tgc	aag	agg	240
Asn	Cys	Gln	His	Asn	Thr	Ala	Gly	Glu	His	Cys	Glu	Arg	Cys	Lys	Arg	
65					70				75						80	
ggg	tac	tat	gga	agc	gcc	atc	cat	gga	tcc	tgc	agg	gtt	tgc	ccc	tgt	288
Gly	Tyr	Tyr	Gly	Ser	Ala	Ile	His	Gly	Ser	Cys	Arg	Val	Cys	Pro	Cys	
				85				90						95		
cct	cac	acc	aac	agc	ttt	gcc	act	ggc	tgt	gct	gtg	gat	gga	gga	gct	336
Pro	His	Thr	Asn	Ser	Phe	Ala	Thr	Gly	Cys	Ala	Val	Asp	Gly	Gly	Ala	
			100					105					110			
gtg	agg	tgt	gcc	tgc	aaa	ccc	gga	tac	aca	gga	gca	cag	tgt	gag	agg	384
Val	Arg	Cys	Ala	Cys	Lys	Pro	Gly	Tyr	Thr	Gly	Ala	Gln	Cys	Glu	Arg	
		115				120						125				
tgt	gca	cca	gga	tat	ttt	ggg	aac	ccc	cag	aaa	ttt	gga	ggg	agc	tgc	432
Cys	Ala	Pro	Gly	Tyr	Phe	Gly	Asn	Pro	Gln	Lys	Phe	Gly	Gly	Ser	Cys	
	130					135					140					
caa	cca	tgc	aat	tgc	aac	agt	aat	ggc	cag	ttt	ggc	act	tgt	gat	ccc	480
Gln	Pro	Cys	Asn	Cys	Asn	Ser	Asn	Gly	Gln	Phe	Gly	Thr	Cys	Asp	Pro	
145					150					155					160	
cta	act	gga	gac	tgt	gta	agc	caa	gaa	ccc	aaa	gat	ggc	agc	cct	gca	528
Leu	Thr	Gly	Asp	Cys	Val	Ser	Gln	Glu	Pro	Lys	Asp	Gly	Ser	Pro	Ala	
				165					170					175		
gaa	gaa	tgt	gat	gac	tgt	gac	agc	tgt	gtg	atg	act	ctc	cta	aat	gac	576
Glu	Glu	Cys	Asp	Asp	Cys	Asp	Ser	Cys	Val	Met	Thr	Leu	Leu	Asn	Asp	
			180					185					190			
ttg	gtc	ccc	atg	ggg	gag	gaa	ctc	gcc	ctg	gtg	aaa	tca	aaa	ctt	cag	624
Leu	Val	Pro	Met	Gly	Glu	Glu	Leu	Ala	Leu	Val	Lys	Ser	Lys	Leu	Gln	
		195					200					205				
ggg	ctg	agt	gtg	aac	act	ggg	tct	ctg	gaa	cag	atc	cgg	cat	gtg	gag	672
Gly	Leu	Ser	Val	Asn	Thr	Gly	Ser	Leu	Glu	Gln	Ile	Arg	His	Val	Glu	

210	215	220	
atg cag gcc aag gac ctg agg aac cag ctg ctt ggc ttc cgt tcc gcc Met Gln Ala Lys Asp L u Arg Asn Gln Leu Leu Gly Phe Arg Ser Ala 225 230 235 240			720
atc tcc agt cac ggg tcc caa atg gac ggc ctg gaa aaa gaa ctc agt Ile Ser Ser His Gly Ser Gln Met Asp Gly Leu Glu Lys Glu Leu Ser 245 250 255			768
cat ttg tac cag gaa ttc gaa act ttg caa gaa aag gcg cag gtc aat His Leu Tyr Gln Glu Phe Glu Thr Leu Gln Glu Lys Ala Gln Val Asn 260 265 270			816
tcc aga aaa gca caa aca tta tat aac aac atc gat acg aca atc caa Ser Arg Lys Ala Gln Thr Leu Tyr Asn Asn Ile Asp Thr Thr Ile Gln 275 280 285			864
aac gcc aaa gag ttg gac atg aag att aaa aac ata ctt acg aat gtg Asn Ala Lys Glu Leu Asp Met Lys Ile Lys Asn Ile Leu Thr Asn Val 290 295 300			912
cac att ctc ctg aag cag atc gct cgg cca ggt gga gaa gga atg gac His Ile Leu Leu Lys Gln Ile Ala Arg Pro Gly Gly Glu Gly Met Asp 305 310 315 320			960
ttg ccg gtg ggc gac tgg tcc agg gag tcg gcg gaa gct cag cgc atg Leu Pro Val Gly Asp Trp Ser Arg Glu Ser Ala Glu Ala Gln Arg Met 325 330 335			1008
ttg cgg gag ctg cga ggc cga gac ttt aaa aag cac ctc caa gaa gca Leu Arg Glu Leu Arg Gly Arg Asp Phe Lys Lys His Leu Gln Glu Ala 340 345 350			1056
gag gcc cag aaa atg gaa gcc cag ctc tta ctg aac cga atc agg acc Glu Ala Gln Lys Met Glu Ala Gln Leu Leu Leu Asn Arg Ile Arg Thr 355 360 365			1104
tgg ctg gaa tcc cac cag gtg gag aac aat gga ctg cta aag aat att Trp Leu Glu Ser His Gln Val Glu Asn Asn Gly Leu Leu Lys Asn Ile 370 375 380			1152
cgg gat tca tta aat gat tat gaa gcc aaa ctt cag gac ctg cgt tcc Arg Asp Ser Leu Asn Asp Tyr Glu Ala Lys Leu Gln Asp Leu Arg Ser 385 390 395 400			1200
gtg ctt cag gag gcg gca gcc cag gga aag cag gct aca ggc ctc aac Val Leu Gln Glu Ala Ala Ala Gln Gly Lys Gln Ala Thr Gly Leu Asn 405 410 415			1248
cac gaa aat gag ggg gtc cta gga gcc atc cag aga caa atg aag gaa His Glu Asn Glu Gly Val Leu Gly Ala Ile Gln Arg Gln Met Lys Glu 420 425 430			1296
atg gat tcc ctg aag aag tac ctc acc gag cac ctg gcc aca gca gac Met Asp Ser Leu Lys Lys Tyr Leu Thr Glu His Leu Ala Thr Ala Asp 435 440 445			1344
gct tcc ctg ctg caa acc aac agt cta ctg cag cgg atg gac acg agc Ala Ser Leu Leu Gln Thr Asn Ser Leu Leu Gln Arg Met Asp Thr S r 450 455 460			1392

cag aag gag tat gaa agc tta gct gct gct tta aac gga gca aga cag	1440
Gln Lys Glu Tyr Glu Ser Leu Ala Ala Ala Leu Asn Gly Ala Arg Gln	
465 470 475 480	
gaa ctg aat gac caa gtg cgg gaa ctc tcc aga tcc gga ggc aaa gca	1488
Glu Leu Asn Asp Gln Val Arg Glu Leu Ser Arg Ser Gly Gly Lys Ala	
485 490 495	
ccc ctg gtg gct gag gcc gag aag cac gct cag tct tta cag gag ctg	1536
Pro Leu Val Ala Glu Ala Glu Lys His Ala Gln Ser Leu Gln Glu Leu	
500 505 510	
gca aag cag ctg gaa gag ata aag aga aac acc agt ggg gat gag tcg	1584
Ala Lys Gln Leu Glu Glu Ile Lys Arg Asn Thr Ser Gly Asp Glu Ser	
515 520 525	
gtg cgc tgt gtc gtg gac gct gcc act gcc tat gag agc atc ctc aac	1632
Val Arg Cys Val Val Asp Ala Ala Thr Ala Tyr Glu Ser Ile Leu Asn	
530 535 540	
gcc atc cga gca gca gag gat gca gcc ggc aag gcc gac agt gcc tca	1680
Ala Ile Arg Ala Ala Glu Asp Ala Ala Gly Lys Ala Asp Ser Ala Ser	
545 550 555 560	
gag tcc gcc ttc cag aca gtg ata aag gaa gat ctt ccg aga aga gcc	1728
Glu Ser Ala Phe Gln Thr Val Ile Lys Glu Asp Leu Pro Arg Arg Ala	
565 570 575	
aaa acc ctg agt tct gac agc gag gaa ctg tta aac gag gcc aag atg	1776
Lys Thr Leu Ser Ser Asp Ser Glu Glu Leu Leu Asn Glu Ala Lys Met	
580 585 590	
aca cgg aaa agg cta cag caa gaa atc aat cca gct ctc aac agc cta	1824
Thr Arg Lys Arg Leu Gln Gln Glu Ile Asn Pro Ala Leu Asn Ser Leu	
595 600 605	
cag caa acc ctg aag act gta tca gtt cag aag gac ctg cta gat gcc	1872
Gln Gln Thr Leu Lys Thr Val Ser Val Gln Lys Asp Leu Leu Asp Ala	
610 615 620	
aat gtc act gct gtc cgt aat gac ctt cgt ggg atc cag aga ggt gat	1920
Asn Val Thr Ala Val Arg Asn Asp Leu Arg Gly Ile Gln Arg Gly Asp	
625 630 635 640	
att gac agt gtg gtg agt gga gcg aag agc atg gtc agg aaa gcc aat	1968
Ile Asp Ser Val Val Ser Gly Ala Lys Ser Met Val Arg Lys Ala Asn	
645 650 655	
ggg ata acg agc gag gtc ctg gac ggg ctc agc ccc atc cag acg gat	2016
Gly Ile Thr Ser Glu Val Leu Asp Gly Leu Ser Pro Ile Gln Thr Asp	
660 665 670	
ttg gga agg att aag gac agc tac ggg agc aca cgg cat gag gac ttc	2064
Leu Gly Arg Ile Lys Asp Ser Tyr Gly Ser Thr Arg His Glu Asp Phe	
675 680 685	
aac aaa gct ctg att gac gcc aat aac tca gta aag aaa tta acc aag	2112
Asn Lys Ala Leu Ile Asp Ala Asn Asn Ser Val Lys Lys Leu Thr Lys	
690 695 700	

aag ttg cct gat ctt ttt gtc aag att gaa agc atc aat caa cag ttg	2160
Lys Leu Pro Asp Leu Phe Val Lys Ile Glu Ser Ile Asn Gln Gln Leu	
705 710 715 720	
ctg ccc ctg gga aac atc tct gac aat gta gac cga atc cga gag ctc	2208
Leu Pro Leu Gly Asn Ile Ser Asp Asn Val Asp Arg Ile Arg Glu Leu	
725 730 735	
att acg cag gcc aga gat gct gcg aac aag gtt gca att ccc atg agg	2256
Ile Thr Gln Ala Arg Asp Ala Ala Asn Lys Val Ala Ile Pro Met Arg	
740 745 750	
ttc aat ggt aaa tct ggt gtt gaa gtc cgt ctg cca aat gac cta gaa	2304
Phe Asn Gly Lys Ser Gly Val Glu Val Arg Leu Pro Asn Asp Leu Glu	
755 760 765	
gac ttg aag gga tac acg tct ctg tct ttg ttc ctc caa aga cca gac	2352
Asp Leu Lys Gly Tyr Thr Ser Leu Ser Leu Phe Leu Gln Arg Pro Asp	
770 775 780	
tta aga gag aat gga ggc act gag gac atg ttt gta atg tac ctt gga	2400
Leu Arg Glu Asn Gly Gly Thr Glu Asp Met Phe Val Met Tyr Leu Gly	
785 790 795 800	
aac aag gat gcc tcc aag gac tac atc ggc atg gcg gtt gta gat ggc	2448
Asn Lys Asp Ala Ser Lys Asp Tyr Ile Gly Met Ala Val Val Asp Gly	
805 810 815	
cag ctg acg tgt gtc tac aac ctg ggg gac cga gaa gct gaa gtt cag	2496
Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu Val Gln	
820 825 830	
atc gat cag gtc ctg acg gag agt gag tct cag gag gca gtt atg gac	2544
Ile Asp Gln Val Leu Thr Glu Ser Glu Ser Gln Glu Ala Val Met Asp	
835 840 845	
cgg gtg aag ttc cag aga ata tat caa ttt gcc aag ctt aat tac acc	2592
Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Lys Leu Asn Tyr Thr	
850 855 860	
aaa gaa gcc acg tcc aat aaa ccc aaa gct ccc gcg gtc tac gac ctg	2640
Lys Glu Ala Thr Ser Asn Lys Pro Lys Ala Pro Ala Val Tyr Asp Leu	
865 870 875 880	
gag ggt ggc agt agc aac acg ctc ctt aat ttg gat ccc gag gac gct	2688
Glu Gly Gly Ser Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu Asp Ala	
885 890 895	
gtg ttt tat gtc gga ggt tac cca ccg gat ttt gaa ctt cct agc aga	2736
Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Glu Leu Pro Ser Arg	
900 905 910	
ctg cgg ttc cct cca tac aaa ggc tgt atc gaa cta gat gac ctc aat	2784
Leu Arg Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp Leu Asn	
915 920 925	
gaa aac gtt cta agc ttg tac aat ttc aag aca act ttc aat ctc aac	2832
Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Thr Thr Phe Asn Leu Asn	
930 935 940	
acc acg gag gtg gag cct tgt agg agg aga aag gaa gag tca gac aaa	2880

Thr	Thr	Glu	Val	Glu	Pro	Cys	Arg	Arg	Arg	Lys	Glu	Glu	Ser	Asp	Lys	
945					950					955					960	
aat	tac	ttt	gaa	ggt	aca	ggc	tat	gct	cgc	atc	cct	act	caa	cca	aat	2928
Asn	Tyr	Phe	Glu	Gly	Thr	Gly	Tyr	Ala	Arg	Ile	Pro	Thr	Gln	Pro	Asn	
				965					970					975		
gct	ccc	ttc	cca	aac	ttc	ata	cag	acc	atc	cag	act	act	gtg	gac	aga	2976
Ala	Pro	Phe	Pro	Asn	Phe	Ile	Gln	Thr	Ile	Gln	Thr	Thr	Val	Asp	Arg	
			980					985					990			
ggt	tta	ctg	ttc	ttc	gca	gaa	aac	cag	gat	aac	ttc	ata	tct	ctg	aac	3024
Gly	Leu	Leu	Phe	Phe	Ala	Glu	Asn	Gln	Asp	Asn	Phe	Ile	Ser	Leu	Asn	
		995					1000					1005				
ata	gaa	gat	ggc	aat	ctc	atg	gtg	aga	tac	aaa	cta	aat	tca	gag	cca	3072
Ile	Glu	Asp	Gly	Asn	Leu	Met	Val	Arg	Tyr	Lys	Leu	Asn	Ser	Glu	Pro	
	1010					1015					1020					
ccc	aaa	gag	aag	gga	att	cga	gac	acc	atc	aac	gat	ggg	aaa	gat	cat	3120
Pro	Lys	Glu	Lys	Gly	Ile	Arg	Asp	Thr	Ile	Asn	Asp	Gly	Lys	Asp	His	
1025					1030					1035				1040		
tcg	atc	tta	atc	aca	att	gga	aaa	cta	caa	aaa	cgc	atg	tgg	ata	aat	3168
Ser	Ile	Leu	Ile	Thr	Ile	Gly	Lys	Leu	Gln	Lys	Arg	Met	Trp	Ile	Asn	
				1045					1050					1055		
gtg	aac	gaa	cgc	agt	gta	cga	atc	gaa	ggg	gaa	ata	ttt	gat	ttc	agc	3216
Val	Asn	Glu	Arg	Ser	Val	Arg	Ile	Glu	Gly	Glu	Ile	Phe	Asp	Phe	Ser	
		1060					1065					1070				
aca	tat	tat	ttg	ggc	gga	att	cca	att	gca	atc	aga	gaa	agg	ttt	aac	3264
Thr	Tyr	Tyr	Leu	Gly	Gly	Ile	Pro	Ile	Ala	Ile	Arg	Glu	Arg	Phe	Asn	
		1075					1080					1085				
atc	tca	acg	cct	gct	ttc	caa	ggc	tgc	atg	aag	aat	ctg	aag	aaa	acc	3312
Ile	Ser	Thr	Pro	Ala	Phe	Gln	Gly	Cys	Met	Lys	Asn	Leu	Lys	Lys	Thr	
	1090					1095					1100					
agt	ggg	gtt	gtc	agg	ttg	aat	gat	act	gtg	ggt	gta	acc	aag	aag	tgc	3360
Ser	Gly	Val	Val	Arg	Leu	Asn	Asp	Thr	Val	Gly	Val	Thr	Lys	Lys	Cys	
1105					1110					1115				1120		
tca	gaa	gac	tgg	aag	ctt	gtg	cga	acc	gcc	tcg	ttc	tcc	aga	gga	ggg	3408
Ser	Glu	Asp	Trp	Lys	Leu	Val	Arg	Thr	Ala	Ser	Phe	Ser	Arg	Gly	Gly	
			1125					1130					1135			
cag	atg	agc	ttt	aca	aac	ttg	gac	gtg	ccc	tcg	act	gac	cgc	ttc	cag	3456
Gln	Met	Ser	Phe	Thr	Asn	Leu	Asp	Val	Pro	Ser	Thr	Asp	Arg	Phe	Gln	
			1140				1145					1150				
ctc	tcc	ttt	ggg	ttt	cag	acc	ttt	caa	ccc	agt	ggc	aca	ctg	ctc	aat	3504
Leu	Ser	Phe	Gly	Phe	Gln	Thr	Phe	Gln	Pro	Ser	Gly	Thr	Leu	Leu	Asn	
		1155				1160						1165				
cat	cag	acg	cgg	aca	agc	agc	ctg	ctg	gtc	acc	ctg	gaa	gat	ggg	cac	3552
His	Gln	Thr	Arg	Thr	Ser	Ser	Leu	Leu	Val	Thr	Leu	Glu	Asp	Gly	His	
	1170					1175				1180						
att	gag	ttg	agc	act	agg	gac	agc	aac	atc	cca	att	ttc	aag	tct	cca	3600
Ile	Glu	Leu	Ser	Thr	Arg	Asp	Ser	Asn	Ile	Pro	Ile	Phe	Lys	Ser	Pro	

1185	1190	1195	1200	
ggg acc tac atg gac ggt tta ctg cat cat gta tct gta ata agt gac				3648
Gly Thr Tyr Met Asp Gly Leu Leu His His Val Ser Val Ile Ser Asp				
	1205	1210	1215	
acc tca ggt ctc cgc ctt ctc atc gat gac cag gtc ctg aga agg aac				3696
Thr Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Val Leu Arg Arg Asn				
	1220	1225	1230	
cag agg ctt cct agc ttc tct aac gcc cag cag tcg ctc cgc ctt gga				3744
Gln Arg Leu Pro Ser Phe Ser Asn Ala Gln Gln Ser Leu Arg Leu Gly				
	1235	1240	1245	
gga ggt cat ttc gag ggt tgt atc agc aat gtt tta gtc caa agg ttt				3792
Gly Gly His Phe Glu Gly Cys Ile Ser Asn Val Leu Val Gln Arg Phe				
	1250	1255	1260	
tca cag agt cca gaa gtc ctg gat ctg gcc agt aaa tct acc aag aag				3840
Ser Gln Ser Pro Glu Val Leu Asp Leu Ala Ser Lys Ser Thr Lys Lys				
	1265	1270	1275	1280
gat gca tcc cta gga ggc tgc agt tta aac aag cca cct ttt ctt atg				3888
Asp Ala Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe Leu Met				
	1285	1290	1295	
ttg ttt aaa agt ccc aag aga ttt aac aag ggc cgg att ttc aat gtt				3936
Leu Phe Lys Ser Pro Lys Arg Phe Asn Lys Gly Arg Ile Phe Asn Val				
	1300	1305	1310	
aat cag ctg atg caa gat gca cct cag gcc aca agg agc aca gag gct				3984
Asn Gln Leu Met Gln Asp Ala Pro Gln Ala Thr Arg Ser Thr Glu Ala				
	1315	1320	1325	
tgg caa gat ggg agg tcc tgc cta cca cct ctg aac acc aag gcc tct				4032
Trp Gln Asp Gly Arg Ser Cys Leu Pro Pro Leu Asn Thr Lys Ala Ser				
	1330	1335	1340	
cac aga gcc ctg cag ttt gga gac agc ccc acc agc cac ttg cta ctc				4080
His Arg Ala Leu Gln Phe Gly Asp Ser Pro Thr Ser His Leu Leu Leu				
	1345	1350	1355	1360
aag ctt ccc cag gaa ctg ctg aaa cct agg tca cag ttt tct tta gac				4128
Lys Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser Gln Phe Ser Leu Asp				
	1365	1370	1375	
ata cag aca act tcc ccc aaa gga ctg gtg ttt tac gca ggc acc aag				4176
Ile Gln Thr Thr Ser Pro Lys Gly Leu Val Phe Tyr Ala Gly Thr Lys				
	1380	1385	1390	
gac tcc ttc ctg gct ctt tat gtc gca gat ggc cgt gtt gtc ttt gct				4224
Asp Ser Phe Leu Ala Leu Tyr Val Ala Asp Gly Arg Val Val Phe Ala				
	1395	1400	1405	
ttg ggg gca gga ggg aag aaa ctg aga ctc agg agc aag gag aga tac				4272
Leu Gly Ala Gly Gly Lys Lys Leu Arg Leu Arg Ser Lys Glu Arg Tyr				
	1410	1415	1420	
cat gac ggg aag tgg cac acg gtg gtg ttc gga cta aat gga gga aag				4320
His Asp Gly Lys Trp His Thr Val Val Phe Gly Leu Asn Gly Gly Lys				
	1425	1430	1435	1440

gca cgc ctg gtt gtg gat ggg cta agg gcc cag gaa ggc agt ttg cct	4368
Ala Arg Leu Val Val Asp Gly Leu Arg Ala Gln Glu Gly Ser Leu Pro	
1445 1450 1455	
gga aat tct acc atc agc ccc aga gaa cag gtt tac cta ggg ttg ccg	4416
Gly Asn Ser Thr Ile Ser Pro Arg Glu Gln Val Tyr Leu Gly Leu Pro	
1460 1465 1470	
cta tca aga aag cca aag agc cta ccc cag cac agt ttt gtg ggg tgc	4464
Leu Ser Arg Lys Pro Lys Ser Leu Pro Gln His Ser Phe Val Gly Cys	
1475 1480 1485	
ctg aga gat ttc cag ttg aac tcg aaa ccc ctg gat tct cct tct gcg	4512
Leu Arg Asp Phe Gln Leu Asn Ser Lys Pro Leu Asp Ser Pro Ser Ala	
1490 1495 1500	
agg ttt ggg gta tct ccc tgc ttg ggt ggc tct tta gag aaa ggc att	4560
Arg Phe Gly Val Ser Pro Cys Leu Gly Gly Ser Leu Glu Lys Gly Ile	
1505 1510 1515 1520	
tat ttc tcc caa gga gga ggc cat gtg atc cta gcc aat tct gtg tcc	4608
Tyr Phe Ser Gln Gly Gly Gly His Val Ile Leu Ala Asn Ser Val Ser	
1525 1530 1535	
ttg ggg cca gag ctt aag ctc act ttc agc att cgc cca cgg agt ctc	4656
Leu Gly Pro Glu Leu Lys Leu Thr Phe Ser Ile Arg Pro Arg Ser Leu	
1540 1545 1550	
act ggg gtc tta ata cac gtc gga agt caa tct gga cag cgc tta agt	4704
Thr Gly Val Leu Ile His Val Gly Ser Gln Ser Gly Gln Arg Leu Ser	
1555 1560 1565	
gtg tac atg gag gca gga aag gtc aca acc tct gtg agc agt gat gca	4752
Val Tyr Met Glu Ala Gly Lys Val Thr Thr Ser Val Ser Ser Asp Ala	
1570 1575 1580	
gga gga agt gtg aca tca att aca ccg aag cag tct ctg tgt gat gga	4800
Gly Gly Ser Val Thr Ser Ile Thr Pro Lys Gln Ser Leu Cys Asp Gly	
1585 1590 1595 1600	
cag tgg cac tcg gtg gca gtc tcc att aaa cag cgc atc ctg cat cta	4848
Gln Trp His Ser Val Ala Val Ser Ile Lys Gln Arg Ile Leu His Leu	
1605 1610 1615	
gaa ctg gat aca gac agt agc tac aca gtc gca cca ctt tcc ttc tca	4896
Glu Leu Asp Thr Asp Ser Ser Tyr Thr Val Ala Pro Leu Ser Phe Ser	
1620 1625 1630	
cca aac agc acc cga ggg tca ctg cac gtc gga ggt gtc cca gac aaa	4944
Pro Asn Ser Thr Arg Gly Ser Leu His Val Gly Gly Val Pro Asp Lys	
1635 1640 1645	
ttg aaa atg ctt aca ctc cct gtg tgg aac tca ttt ttt ggc tgt ctg	4992
Leu Lys Met Leu Thr Leu Pro Val Trp Asn Ser Phe Phe Gly Cys Leu	
1650 1655 1660	
aag aat att caa gtc aac cat gtc cct gtc ccc atc aca gaa gcc aca	5040
Lys Asn Ile Gln Val Asn His Val Pro Val Pro Ile Thr Glu Ala Thr	
1665 1670 1675 1680	

gaa gtc caa ggt tct gtc agc ctg aat ggc tgc cct gac cac
 Glu Val Gln Gly Ser Val Ser Leu Asn Gly Cys Pro Asp His
 1685 1690

5082

taaccctaca cagcaagatt cacctttgga g

5113

<210> 12

<211> 1694

<212> PRT

<213> Rattus norvegicus

<400> 12

Gln Gln Arg Val Ala Phe Leu Gln His Pro Gly Gln Asn His Leu Gln
 1 5 10 15

Ala Ser Tyr Met Glu Leu Arg Pro Ser Gln Gly Cys Arg Pro Gly Tyr
 20 25 30

Tyr Arg Asp Ile Lys Ser Phe Pro Ala Gly Arg Ser Val Pro Cys Asn
 35 40 45

Cys Asn Gly His Ser Asn Arg Cys Gln Asp Gly Ser Gly Val Cys Ile
 50 55 60

Asn Cys Gln His Asn Thr Ala Gly Glu His Cys Glu Arg Cys Lys Arg
 65 70 75 80

Gly Tyr Tyr Gly Ser Ala Ile His Gly Ser Cys Arg Val Cys Pro Cys
 85 90 95

Pro His Thr Asn Ser Phe Ala Thr Gly Cys Ala Val Asp Gly Gly Ala
 100 105 110

Val Arg Cys Ala Cys Lys Pro Gly Tyr Thr Gly Ala Gln Cys Glu Arg
 115 120 125

Cys Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe Gly Gly Ser Cys
 130 135 140

Gln Pro Cys Asn Cys Asn Ser Asn Gly Gln Phe Gly Thr Cys Asp Pro
 145 150 155 160

Leu Thr Gly Asp Cys Val Ser Gln Glu Pro Lys Asp Gly Ser Pro Ala
 165 170 175

Glu Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr Leu Leu Asn Asp
 180 185 190

Leu Val Pro Met Gly Glu Glu Leu Ala Leu Val Lys Ser Lys Leu Gln
 195 200 205

Gly Leu Ser Val Asn Thr Gly Ser Leu Glu Gln Ile Arg His Val Glu
 210 215 220

Met Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Gly Phe Arg Ser Ala
 225 230 235 240

Ile Ser Ser His Gly Ser Gln Met Asp Gly Leu Glu Lys Glu Leu Ser
 245 250 255

His Leu Tyr Gln Glu Phe Glu Thr Leu Gln Glu Lys Ala Gln Val Asn
260 265 270

Ser Arg Lys Ala Gln Thr Leu Tyr Asn Asn Ile Asp Thr Thr Ile Gln
275 280 285

Asn Ala Lys Glu Leu Asp Met Lys Ile Lys Asn Ile Leu Thr Asn Val
290 295 300

His Ile Leu Leu Lys Gln Ile Ala Arg Pro Gly Gly Glu Gly Met Asp
305 310 315 320

Leu Pro Val Gly Asp Trp Ser Arg Glu Ser Ala Glu Ala Gln Arg Met
325 330 335

Leu Arg Glu Leu Arg Gly Arg Asp Phe Lys Lys His Leu Gln Glu Ala
340 345 350

Glu Ala Gln Lys Met Glu Ala Gln Leu Leu Leu Asn Arg Ile Arg Thr
355 360 365

Trp Leu Glu Ser His Gln Val Glu Asn Asn Gly Leu Leu Lys Asn Ile
370 375 380

Arg Asp Ser Leu Asn Asp Tyr Glu Ala Lys Leu Gln Asp Leu Arg Ser
385 390 395 400

Val Leu Gln Glu Ala Ala Ala Gln Gly Lys Gln Ala Thr Gly Leu Asn
405 410 415

His Glu Asn Glu Gly Val Leu Gly Ala Ile Gln Arg Gln Met Lys Glu
420 425 430

Met Asp Ser Leu Lys Lys Tyr Leu Thr Glu His Leu Ala Thr Ala Asp
435 440 445

Ala Ser Leu Leu Gln Thr Asn Ser Leu Leu Gln Arg Met Asp Thr Ser
450 455 460

Gln Lys Glu Tyr Glu Ser Leu Ala Ala Ala Leu Asn Gly Ala Arg Gln
465 470 475 480

Glu Leu Asn Asp Gln Val Arg Glu Leu Ser Arg Ser Gly Gly Lys Ala
485 490 495

Pro Leu Val Ala Glu Ala Glu Lys His Ala Gln Ser Leu Gln Glu Leu
500 505 510

Ala Lys Gln Leu Glu Glu Ile Lys Arg Asn Thr Ser Gly Asp Glu Ser
515 520 525

Val Arg Cys Val Val Asp Ala Ala Thr Ala Tyr Glu Ser Ile Leu Asn
530 535 540

Ala Ile Arg Ala Ala Glu Asp Ala Ala Gly Lys Ala Asp Ser Ala Ser
545 550 555 560

Glu Ser Ala Phe Gln Thr Val Ile Lys Glu Asp Leu Pro Arg Arg Ala
565 570 575

Lys Thr Leu Ser Ser Asp Ser Glu Glu Leu Leu Asn Glu Ala Lys Met

580					585					590					
Thr	Arg	Lys	Arg	Leu	Gln	Gln	Glu	Ile	Asn	Pro	Ala	Leu	Asn	Ser	Leu
		595					600					605			
Gln	Gln	Thr	Leu	Lys	Thr	Val	Ser	Val	Gln	Lys	Asp	Leu	Leu	Asp	Ala
		610					615					620			
Asn	Val	Thr	Ala	Val	Arg	Asn	Asp	Leu	Arg	Gly	Ile	Gln	Arg	Gly	Asp
		625					630					635			640
Ile	Asp	Ser	Val	Val	Ser	Gly	Ala	Lys	Ser	Met	Val	Arg	Lys	Ala	Asn
				645					650					655	
Gly	Ile	Thr	Ser	Glu	Val	Leu	Asp	Gly	Leu	Ser	Pro	Ile	Gln	Thr	Asp
			660					665						670	
Leu	Gly	Arg	Ile	Lys	Asp	Ser	Tyr	Gly	Ser	Thr	Arg	His	Glu	Asp	Phe
		675					680					685			
Asn	Lys	Ala	Leu	Ile	Asp	Ala	Asn	Asn	Ser	Val	Lys	Lys	Leu	Thr	Lys
		690					695					700			
Lys	Leu	Pro	Asp	Leu	Phe	Val	Lys	Ile	Glu	Ser	Ile	Asn	Gln	Gln	Leu
		705					710					715			720
Leu	Pro	Leu	Gly	Asn	Ile	Ser	Asp	Asn	Val	Asp	Arg	Ile	Arg	Glu	Leu
			725						730					735	
Ile	Thr	Gln	Ala	Arg	Asp	Ala	Ala	Asn	Lys	Val	Ala	Ile	Pro	Met	Arg
			740						745					750	
Phe	Asn	Gly	Lys	Ser	Gly	Val	Glu	Val	Arg	Leu	Pro	Asn	Asp	Leu	Glu
		755					760					765			
Asp	Leu	Lys	Gly	Tyr	Thr	Ser	Leu	Ser	Leu	Phe	Leu	Gln	Arg	Pro	Asp
		770					775					780			
Leu	Arg	Glu	Asn	Gly	Gly	Thr	Glu	Asp	Met	Phe	Val	Met	Tyr	Leu	Gly
		785					790					795			800
Asn	Lys	Asp	Ala	Ser	Lys	Asp	Tyr	Ile	Gly	Met	Ala	Val	Val	Asp	Gly
			805						810					815	
Gln	Leu	Thr	Cys	Val	Tyr	Asn	Leu	Gly	Asp	Arg	Glu	Ala	Glu	Val	Gln
			820						825					830	
Ile	Asp	Gln	Val	Leu	Thr	Glu	Ser	Glu	Ser	Gln	Glu	Ala	Val	Met	Asp
			835						840					845	
Arg	Val	Lys	Phe	Gln	Arg	Ile	Tyr	Gln	Phe	Ala	Lys	Leu	Asn	Tyr	Thr
			850				855					860			
Lys	Glu	Ala	Thr	Ser	Asn	Lys	Pro	Lys	Ala	Pro	Ala	Val	Tyr	Asp	Leu
		865					870					875			880
Glu	Gly	Gly	Ser	Ser	Asn	Thr	Leu	Leu	Asn	Leu	Asp	Pro	Glu	Asp	Ala
			885						890					895	
Val	Phe	Tyr	Val	Gly	Gly	Tyr	Pro	Pro	Asp	Phe	Glu	Leu	Pro	Ser	Arg
			900				905						910		

Leu Arg Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp Leu Asn
915 920 925

Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Thr Thr Phe Asn Leu Asn
930 935 940

Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser Asp Lys
945 950 955 960

Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Ile Pro Thr Gln Pro Asn
965 970 975

Ala Pro Phe Pro Asn Phe Ile Gln Thr Ile Gln Thr Thr Val Asp Arg
980 985 990

Gly Leu Leu Phe Phe Ala Glu Asn Gln Asp Asn Phe Ile Ser Leu Asn
995 1000 1005

Ile Glu Asp Gly Asn Leu Met Val Arg Tyr Lys Leu Asn Ser Glu Pro
1010 1015 1020

Pro Lys Glu Lys Gly Ile Arg Asp Thr Ile Asn Asp Gly Lys Asp His
1025 1030 1035 1040

Ser Ile Leu Ile Thr Ile Gly Lys Leu Gln Lys Arg Met Trp Ile Asn
1045 1050 1055

Val Asn Glu Arg Ser Val Arg Ile Glu Gly Glu Ile Phe Asp Phe Ser
1060 1065 1070

Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg Phe Asn
1075 1080 1085

Ile Ser Thr Pro Ala Phe Gln Gly Cys Met Lys Asn Leu Lys Lys Thr
1090 1095 1100

Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys Lys Cys
1105 1110 1115 1120

Ser Glu Asp Trp Lys Leu Val Arg Thr Ala Ser Phe Ser Arg Gly Gly
1125 1130 1135

Gln Met Ser Phe Thr Asn Leu Asp Val Pro Ser Thr Asp Arg Phe Gln
1140 1145 1150

Leu Ser Phe Gly Phe Gln Thr Phe Gln Pro Ser Gly Thr Leu Leu Asn
1155 1160 1165

His Gln Thr Arg Thr Ser Ser Leu Leu Val Thr Leu Glu Asp Gly His
1170 1175 1180

Ile Glu Leu Ser Thr Arg Asp Ser Asn Ile Pro Ile Phe Lys Ser Pro
1185 1190 1195 1200

Gly Thr Tyr Met Asp Gly Leu Leu His His Val Ser Val Ile Ser Asp
1205 1210 1215

Thr Ser Gly Leu Arg Leu Leu Ile Asp Asp Gln Val Leu Arg Arg Asn
1220 1225 1230

Gln Arg Leu Pro Ser Phe Ser Asn Ala Gln Gln Ser Leu Arg Leu Gly
1235 1240 1245

Gly Gly His Phe Glu Gly Cys Ile Ser Asn Val Leu Val Gln Arg Phe
1250 1255 1260

Ser Gln Ser Pro Glu Val Leu Asp Leu Ala Ser Lys Ser Thr Lys Lys
1265 1270 1275 1280

Asp Ala Ser Leu Gly Gly Cys Ser Leu Asn Lys Pro Pro Phe Leu Met
1285 1290 1295

Leu Phe Lys Ser Pro Lys Arg Phe Asn Lys Gly Arg Ile Phe Asn Val
1300 1305 1310

Asn Gln Leu Met Gln Asp Ala Pro Gln Ala Thr Arg Ser Thr Glu Ala
1315 1320 1325

Trp Gln Asp Gly Arg Ser Cys Leu Pro Pro Leu Asn Thr Lys Ala Ser
1330 1335 1340

His Arg Ala Leu Gln Phe Gly Asp Ser Pro Thr Ser His Leu Leu Leu
1345 1350 1355 1360

Lys Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser Gln Phe Ser Leu Asp
1365 1370 1375

Ile Gln Thr Thr Ser Pro Lys Gly Leu Val Phe Tyr Ala Gly Thr Lys
1380 1385 1390

Asp Ser Phe Leu Ala Leu Tyr Val Ala Asp Gly Arg Val Val Phe Ala
1395 1400 1405

Leu Gly Ala Gly Gly Lys Lys Leu Arg Leu Arg Ser Lys Glu Arg Tyr
1410 1415 1420

His Asp Gly Lys Trp His Thr Val Val Phe Gly Leu Asn Gly Gly Lys
1425 1430 1435 1440

Ala Arg Leu Val Val Asp Gly Leu Arg Ala Gln Glu Gly Ser Leu Pro
1445 1450 1455

Gly Asn Ser Thr Ile Ser Pro Arg Glu Gln Val Tyr Leu Gly Leu Pro
1460 1465 1470

Leu Ser Arg Lys Pro Lys Ser Leu Pro Gln His Ser Phe Val Gly Cys
1475 1480 1485

Leu Arg Asp Phe Gln Leu Asn Ser Lys Pro Leu Asp Ser Pro Ser Ala
1490 1495 1500

Arg Phe Gly Val Ser Pro Cys Leu Gly Gly Ser Leu Glu Lys Gly Ile
1505 1510 1515 1520

Tyr Phe Ser Gln Gly Gly Gly His Val Ile Leu Ala Asn Ser Val Ser
1525 1530 1535

Leu Gly Pro Glu Leu Lys Leu Thr Phe Ser Ile Arg Pro Arg Ser Leu
1540 1545 1550

Thr Gly Val Leu Ile His Val Gly Ser Gln Ser Gly Gln Arg Leu Ser

1555 1560 1565
 Val Tyr Met Glu Ala Gly Lys Val Thr Thr Ser Val Ser Ser Asp Ala
 1570 1575 1580
 Gly Gly Ser Val Thr Ser Ile Thr Pro Lys Gln Ser Leu Cys Asp Gly
 1585 1590 1595 1600
 Gln Trp His Ser Val Ala Val Ser Ile Lys Gln Arg Ile Leu His Leu
 1605 1610 1615
 Glu Leu Asp Thr Asp Ser Ser Tyr Thr Val Ala Pro Leu Ser Phe Ser
 1620 1625 1630
 Pro Asn Ser Thr Arg Gly Ser Leu His Val Gly Gly Val Pro Asp Lys
 1635 1640 1645
 Leu Lys Met Leu Thr Leu Pro Val Trp Asn Ser Phe Phe Gly Cys Leu
 1650 1655 1660
 Lys Asn Ile Gln Val Asn His Val Pro Val Pro Ile Thr Glu Ala Thr
 1665 1670 1675 1680
 Glu Val Gln Gly Ser Val Ser Leu Asn Gly Cys Pro Asp His
 1685 1690

<210> 13
 <211> 3930
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (121)..(3630)

<220>
 <221> sig_peptide
 <222> (121)..(171)

<400> 13
 gggcgggagg aggactgtat ctctggatgc ctggggcctg gtttcagggc ctgatttatt 60
 cctcttcctg ggagctcact caggaaaggt cctttctggg gatcacccca ttggctgaag 120
 atg aga cca ttc ttc ctc ttg tgt ttt gcc ctg cct ggc ctc ctg cat 168
 Met Arg Pro Phe Phe Leu Leu Cys Phe Ala Leu Pro Gly Leu Leu His
 1 5 10 15
 gcc caa caa gcc tgc tcc cgt ggg gcc tgc tat cca cct gtt ggg gac 216
 Ala Gln Gln Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp
 20 25 30
 ctg ctt gtt ggg agg acc cgg ttt ctc cga gct tca tct acc tgt gga 264
 Leu Leu Val Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly
 35 40 45
 ctg acc aag cct gag acc tac tgc acc cag tat ggc gag tgg cag atg 312
 Leu Thr Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met
 50 55 60

aaa tgc tgc aag tgt gac tcc agg cag cct cac aac tac tac agt cac	360
Lys Cys Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His	
65 70 75 80	
cga gta gag aat gtg gct tca tcc tcc ggc ccc atg cgc tgg tgg cag	408
Arg Val Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln	
85 90 95	
tcc cag aat gat gtg aac cct gtc tct ctg cag ctg gac ctg gac agg	456
Ser Gln Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg	
100 105 110	
aga ttc cag ctt caa gaa gtc atg atg gag ttc cga ggg ccc atg cct	504
Arg Phe Gln Leu Gln Glu Val Met Met Glu Phe Arg Gly Pro Met Pro	
115 120 125	
gcc ggc atg ctg att gag cgc tcc tca gac ttc ggt aag acc tgg cga	552
Ala Gly Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg	
130 135 140	
gtg tac cag tac ctg gct gcc gac tgc acc tcc acc ttc cct cgg gtc	600
Val Tyr Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val	
145 150 155 160	
cgc cag ggt cgg cct cag agc tgg cag gat gtt cgg tgc cag tcc ctg	648
Arg Gln Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu	
165 170 175	
cct cag agg cct aat gca cgc cta aat ggg ggg aag gtc caa ctt aac	696
Pro Gln Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn	
180 185 190	
ctt atg gat tta gtg tct ggg att cca gca act caa agt caa aaa att	744
Leu Met Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile	
195 200 205	
caa gag gtg ggg gag atc aca aac ttg aga gtc aat ttc acc agg ctg	792
Gln Glu Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu	
210 215 220	
gcc cct gtg ccc caa agg ggc tac cac cct ccc agc gcc tac tat gct	840
Ala Pro Val Pro Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala	
225 230 235 240	
gtg tcc cag ctc cgt ctg cag ggg agc tgc ttc tgt cac ggc cat gct	888
Val Ser Gln Leu Arg Leu Gln Gly Ser Cys Phe Cys His Gly His Ala	
245 250 255	
gat cgc tgc gca ccc aag cct ggg gcc tct gca ggc tcc acc gct gtg	936
Asp Arg Cys Ala Pro Lys Pro Gly Ala Ser Ala Gly Ser Thr Ala Val	
260 265 270	
cag gtc cac gat gtc tgc gtc tgc cag cac aac act gcc ggc cca aat	984
Gln Val His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro Asn	
275 280 285	
tgt gag cgc tgt gca ccc ttc tac aac aac cgg ccc tgg aga ccg gcg	1032
Cys Glu Arg Cys Ala Pro Phe Tyr Asn Asn Arg Pro Trp Arg Pro Ala	
290 295 300	
gag ggc cag gac gcc cat gaa tgc caa agg tgc gac tgc aat ggg cac	1080

Glu Gly Gln Asp Ala His Glu Cys Gln Arg Cys Asp Cys Asn Gly His	
305 310 315 320	
tca gag aca tgt cac ttt gac ccc gct gtg ttt gcc gcc agc cag ggg	1128
Ser Glu Thr Cys His Phe Asp Pro Ala Val Phe Ala Ala Ser Gln Gly	
325 330 335	
gca tat gga ggt gtg tgt gac aat tgc cgg gac cac acc gaa ggc aag	1176
Ala Tyr Gly Gly Val Cys Asp Asn Cys Arg Asp His Thr Glu Gly Lys	
340 345 350	
aac tgt gag cgg tgt cag ctg cac tat ttc cgg aac cgg cgc ccg gga	1224
Asn Cys Glu Arg Cys Gln Leu His Tyr Phe Arg Asn Arg Arg Pro Gly	
355 360 365	
gct tcc att cag gag acc tgc atc tcc tgc gag tgt gat ccg gat ggg	1272
Ala Ser Ile Gln Glu Thr Cys Ile Ser Cys Glu Cys Asp Pro Asp Gly	
370 375 380	
gca gtc gca ggg gct ccc tgt gac cca gtg acc ggg cag tgt gtg tgc	1320
Ala Val Ala Gly Ala Pro Cys Asp Pro Val Thr Gly Gln Cys Val Cys	
385 390 395 400	
aag gag cat gtg cag gga gag cgc tgt gac cta tgc aag ccg ggc ttc	1368
Lys Glu His Val Gln Gly Glu Arg Cys Asp Leu Cys Lys Pro Gly Phe	
405 410 415	
act gga ctc acc tac gcc aac ccg cga cgg tgc cac cgc tgt gac tgc	1416
Thr Gly Leu Thr Tyr Ala Asn Pro Arg Arg Cys His Arg Cys Asp Cys	
420 425 430	
aac atc ctg ggg tcc cgg gag atg ccg tgt gac gag gag agt ggg cgc	1464
Asn Ile Leu Gly Ser Arg Glu Met Pro Cys Asp Glu Glu Ser Gly Arg	
435 440 445	
tgc ctt tgt ctg ccc aac gtg gtg ggt ccc aaa tgt gac cag tgt gct	1512
Cys Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln Cys Ala	
450 455 460	
ccc tac cac tgg aag ctg gcc agt ggc cag ggc tgt gaa ccg tgt gcc	1560
Pro Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys Ala	
465 470 475 480	
tgc gac ccg cac aac tcc ctc agc cca cag tgc aac cag ttc aca ggg	1608
Cys Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn Gln Phe Thr Gly	
485 490 495	
cag tgc ccc tgt cgg gaa ggc ttt ggt ggc ctg atg tgc agc gct gca	1656
Gln Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met Cys Ser Ala Ala	
500 505 510	
gcc atc cgc cag tgt cca gac cgg acc tat gga gac gtg gcc aca gga	1704
Ala Ile Arg Gln Cys Pro Asp Arg Thr Tyr Gly Asp Val Ala Thr Gly	
515 520 525	
tgc cga gcc tgt gac tgt gat ttc cgg gga aca gag ggc ccg ggc tgc	1752
Cys Arg Ala Cys Asp Cys Asp Phe Arg Gly Thr Glu Gly Pro Gly Cys	
530 535 540	
gac aag gca tca ggc cgc tgc ctc tgc cgc cct ggc ttg acc ggg ccc	1800
Asp Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly Leu Thr Gly Pro	

545	550	555	560	
cgc tgt gac cag tgc cag cga ggc tac tgc aat cgc tac ccg gtg tgc				1848
Arg Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg Tyr Pro Val Cys				
	565	570	575	
gtg gcc tgc cac cct tgc ttc cag acc tat gat gcg gac ctc cgg gag				1896
Val Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu Arg Glu				
	580	585	590	
cag gcc ctg cgc ttt ggt aga ctc ccg aat gcc acc gcc agc ctg tgg				1944
Gln Ala Leu Arg Phe Gly Arg Leu Pro Asn Ala Thr Ala Ser Leu Trp				
	595	600	605	
tca ggg cct ggg ctg gag gac cgt ggc ctg gcc tcc cgg atc cta gat				1992
Ser Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile Leu Asp				
	610	615	620	
gca aag agt aag att gag cag atc cga gca gtt ctc agc agc ccc gca				2040
Ala Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser Pro Ala				
	625	630	635	640
gtc aca gag cag gag gtg gct cag gtg gcc agt gcc atc ctc tcc ctc				2088
Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu Ser Leu				
	645	650	655	
agg cga act ctc cag ggc ctg cag ctg gat ctg ccc ctg gag gag gag				2136
Arg Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu Glu				
	660	665	670	
acg ttg tcc ctt ccg aga gac ctg gag agt ctt gac aga agc ttc aat				2184
Thr Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe Asn				
	675	680	685	
ggt ctc ctt act atg tat cag agg aag agg gag cag ttt gaa aaa ata				2232
Gly Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys Ile				
	690	695	700	
agc agt gct gat cct tca gga gcc ttc ccg atg ctg agc aca gcc tac				2280
Ser Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu Ser Thr Ala Tyr				
	705	710	715	720
gag cag tca gcc cag gct gct cag cag gtc tcc gac agc tcg cgc ctt				2328
Glu Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser Arg Leu				
	725	730	735	
ttg gac cag ctc agg gac agc ccg aga gag gca gag agg ctg gtg cgg				2376
Leu Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu Val Arg				
	740	745	750	
cag gcg gga gga gga gga ggc acc ggc agc ccc aag ctt gtg gcc ctg				2424
Gln Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val Ala Leu				
	755	760	765	
agg ttg gag atg tct tcg ttg cct gac ctg aca ccc acc ttc aac aag				2472
Arg Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe Asn Lys				
	770	775	780	
ctc tgt ggc aac tcc agg cag atg gct tgc acc cca ata tca tgc cct				2520
Leu Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser Cys Pro				
	785	790	795	800

ggt gag cta tgt ccc caa gac aat ggc aca gcc tgt gcg tcc cgc tgc	2568
Gly Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys Ala Ser Arg Cys	
805 810 815	
agg ggt gtc ctt ccc agg gcc ggt ggg gcc ttc ttg atg gcg ggg cag	2616
Arg Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu Met Ala Gly Gln	
820 825 830	
gtg gct gag cag ctg cgg ggc ttc aat gcc cag ctc cag cgg acc agg	2664
Val Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr Arg	
835 840 845	
cag atg att agg gca gcc gag gaa tct gcc tca cag att caa tcc agt	2712
Gln Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser Ser	
850 855 860	
gcc cag cgc ttg gag acc cag gtg agc gcc agc cgc tcc cag atg gag	2760
Ala Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg Ser Gln Met Glu	
865 870 875 880	
gaa gat gtc aga cgc aca cgg ctc cta atc cag cag gtc cgg gac ttc	2808
Glu Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln Val Arg Asp Phe	
885 890 895	
cta aca gac ccc gac act gat gca gcc act atc cag gag gtc agc gag	2856
Leu Thr Asp Pro Asp Thr Asp Ala Ala Thr Ile Gln Glu Val Ser Glu	
900 905 910	
gcc gtg ctg gcc ctg tgg ctg ccc aca gac tca gct act gtt ctg cag	2904
Ala Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala Thr Val Leu Gln	
915 920 925	
aag atg aat gag atc cag gcc att gca gcc agg ctc ccc aac gtg gac	2952
Lys Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu Pro Asn Val Asp	
930 935 940	
ttg gtg ctg tcc cag acc aag cag gac att gcg cgt gcc cgc cgg ttg	3000
Leu Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg Leu	
945 950 955 960	
cag gct gag gct gag gaa gcc agg agc cga gcc cat gca gtg gag ggc	3048
Gln Ala Glu Ala Glu Glu Ala Arg Ser Arg Ala His Ala Val Glu Gly	
965 970 975	
cag gtg gag gat gtg gtt ggg aac ctg cgg cag ggg aca gtg gca ctg	3096
Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val Ala Leu	
980 985 990	
cag gaa gct cag gac acc atg caa ggc acc agc cgg tcc ctt cgg ctt	3144
Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu Arg Leu	
995 1000 1005	
atc cag gac agg gtt gct gag gtt cag cag gta ctg cgg cca gca gaa	3192
Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro Ala Glu	
1010 1015 1020	
aag ctg gtg aca agc atg acc aag cag ctg ggt gac ttc tgg aca cgg	3240
Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp Thr Arg	
1025 1030 1035 1040	

atg gag gag ctc cgc cac caa gcc cgg cag cag ggg gca gag gca gtc 3288
 Met Glu Glu Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu Ala Val
 1045 1050 1055
 cag gcc cag cag ctt gcg gaa ggt gcc agc gag cag gca ttg agt gcc 3336
 Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln Ala Leu Ser Ala
 1060 1065 1070
 caa gag gga ttt gag aga ata aaa caa aag tat gct gag ttg aag gac 3384
 Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys Asp
 1075 1080 1085
 cgg ttg ggt cag agt tcc atg ctg ggt gag cag ggt gcc cgg atc cag 3432
 Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg Ile Gln
 1090 1095 1100
 agt gtg aag aca gag gca gag gag ctg ttt ggg gag acc atg gag atg 3480
 Ser Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu Thr Met Glu Met
 1105 1110 1115 1120
 atg gac agg atg aaa gac atg gag ttg gag ctg ctg cgg ggc agc cag 3528
 Met Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu Arg Gly Ser Gln
 1125 1130 1135
 gcc atc atg ctg cgc tca gcg gac ctg aca gga ctg gag aag cgt gtg 3576
 Ala Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu Glu Lys Arg Val
 1140 1145 1150
 gag cag atc cgt gac cac atc aat ggg cgc gtg ctc tac tat gcc acc 3624
 Glu Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu Tyr Tyr Ala Thr
 1155 1160 1165
 tgc aag tgatgctaca cggtccagcc cggtgccccca ctcatctgcg cgcttttgctt 3680
 Cys Lys
 1170
 ttgggttgggg ggcagattgg gttggaatgc tttccatctc caggagactt tcatgtagcc 3740
 caaagtacag cctggaccac ccctggtgtg ttagctagt aagattaccc tgagctgcag 3800
 ctgagcctga gccaatggga cagttacact tgacagacaa agatggtgga gattggcatg 3860
 ccattgaaac taagagctct caagtcaagg aagctgggct gggcagtatc cccgcctttt 3920
 agttctccac 3930

<210> 14
 <211> 1170
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Arg Pro Phe Phe Leu Leu Cys Phe Ala Leu Pro Gly Leu Leu His
 1 5 10 15
 Ala Gln Gln Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp
 20 25 30
 Leu Leu Val Gly Arg Thr Arg Phe L u Arg Ala Ser Ser Thr Cys Gly
 35 40 45

Leu Thr Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met
 50 55 60
 Lys Cys Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His
 65 70 75 80
 Arg Val Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln
 85 90 95
 Ser Gln Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg
 100 105 110
 Arg Phe Gln Leu Gln Glu Val Met Met Glu Phe Arg Gly Pro Met Pro
 115 120 125
 Ala Gly Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg
 130 135 140
 Val Tyr Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val
 145 150 155 160
 Arg Gln Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu
 165 170 175
 Pro Gln Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn
 180 185 190
 Leu Met Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile
 195 200 205
 Gln Glu Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu
 210 215 220
 Ala Pro Val Pro Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala
 225 230 235 240
 Val Ser Gln Leu Arg Leu Gln Gly Ser Cys Phe Cys His Gly His Ala
 245 250 255
 Asp Arg Cys Ala Pro Lys Pro Gly Ala Ser Ala Gly Ser Thr Ala Val
 260 265 270
 Gln Val His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro Asn
 275 280 285
 Cys Glu Arg Cys Ala Pro Phe Tyr Asn Asn Arg Pro Trp Arg Pro Ala
 290 295 300
 Glu Gly Gln Asp Ala His Glu Cys Gln Arg Cys Asp Cys Asn Gly His
 305 310 315 320
 Ser Glu Thr Cys His Phe Asp Pro Ala Val Phe Ala Ala Ser Gln Gly
 325 330 335
 Ala Tyr Gly Gly Val Cys Asp Asn Cys Arg Asp His Thr Glu Gly Lys
 340 345 350
 Asn Cys Glu Arg Cys Gln Leu His Tyr Phe Arg Asn Arg Arg Pro Gly
 355 360 365

Ala Ser Ile Gln Glu Thr Cys Ile Ser Cys Glu Cys Asp Pro Asp Gly
370 375 380

Ala Val Ala Gly Ala Pro Cys Asp Pro Val Thr Gly Gln Cys Val Cys
385 390 395 400

Lys Glu His Val Gln Gly Glu Arg Cys Asp Leu Cys Lys Pro Gly Phe
405 410 415

Thr Gly Leu Thr Tyr Ala Asn Pro Arg Arg Cys His Arg Cys Asp Cys
420 425 430

Asn Ile Leu Gly Ser Arg Glu Met Pro Cys Asp Glu Glu Ser Gly Arg
435 440 445

Cys Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln Cys Ala
450 455 460

Pro Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys Ala
465 470 475 480

Cys Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn Gln Phe Thr Gly
485 490 495

Gln Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met Cys Ser Ala Ala
500 505 510

Ala Ile Arg Gln Cys Pro Asp Arg Thr Tyr Gly Asp Val Ala Thr Gly
515 520 525

Cys Arg Ala Cys Asp Cys Asp Phe Arg Gly Thr Glu Gly Pro Gly Cys
530 535 540

Asp Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly Leu Thr Gly Pro
545 550 555 560

Arg Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg Tyr Pro Val Cys
565 570 575

Val Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu Arg Glu
580 585 590

Gln Ala Leu Arg Phe Gly Arg Leu Pro Asn Ala Thr Ala Ser Leu Trp
595 600 605

Ser Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile Leu Asp
610 615 620

Ala Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser Pro Ala
625 630 635 640

Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu Ser Leu
645 650 655

Arg Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu Glu
660 665 670

Thr Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe Asn
675 680 685

Gly Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys Ile

690 695 700
Ser Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu Ser Thr Ala Tyr
705 710 715 720
Glu Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser Arg Leu
725 730 735
Leu Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu Val Arg
740 745 750
Gln Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val Ala Leu
755 760 765
Arg Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe Asn Lys
770 775 780
Leu Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser Cys Pro
785 790 795 800
Gly Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys Ala Ser Arg Cys
805 810 815
Arg Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu Met Ala Gly Gln
820 825 830
Val Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr Arg
835 840 845
Gln Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser Ser
850 855 860
Ala Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg Ser Gln Met Glu
865 870 875 880
Glu Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln Val Arg Asp Phe
885 890 895
Leu Thr Asp Pro Asp Thr Asp Ala Ala Thr Ile Gln Glu Val Ser Glu
900 905 910
Ala Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala Thr Val Leu Gln
915 920 925
Lys Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu Pro Asn Val Asp
930 935 940
Leu Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg Leu
945 950 955 960
Gln Ala Glu Ala Glu Glu Ala Arg Ser Arg Ala His Ala Val Glu Gly
965 970 975
Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val Ala Leu
980 985 990
Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu Arg Leu
995 1000 1005
Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro Ala Glu
1010 1015 1020

Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp Thr Arg
 1025 1030 1035 1040
 Met Glu Glu Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu Ala Val
 1045 1050 1055
 Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln Ala Leu Ser Ala
 1060 1065 1070
 Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys Asp
 1075 1080 1085
 Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg Ile Gln
 1090 1095 1100
 Ser Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu Thr Met Glu Met
 1105 1110 1115 1120
 Met Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu Arg Gly Ser Gln
 1125 1130 1135
 Ala Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu Glu Lys Arg Val
 1140 1145 1150
 Glu Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu Tyr Tyr Ala Thr
 1155 1160 1165
 Cys Lys
 1170

<210> 15
 <211> 3759
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(3459)

<400> 15
 caa caa gcc tgc tcc cgt ggg gcc tgc tat cca cct gtt ggg gac ctg 48
 Gln Gln Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu
 1 5 10 15
 ctt gtt ggg agg acc cgg ttt ctc cga gct tca tct acc tgt gga ctg 96
 Leu Val Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu
 20 25 30
 acc aag cct gag acc tac tgc acc cag tat ggc gag tgg cag atg aaa 144
 Thr Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys
 35 40 45
 tgc tgc aag tgt gac tcc agg cag cct cac aac tac tac agt cac cga 192
 Cys Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His Arg
 50 55 60
 gta gag aat gtg gct tca tcc tcc ggc ccc atg cgc tgg tgg cag tcc 240
 Val Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln Ser
 65 70 75 80

cag aat gat gtg aac cct gtc tct ctg cag ctg gac ctg gac agg aga	288
Gln Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg Arg	
85 90 95	
ttc cag ctt caa gaa gtc atg atg gag ttc cga ggg ccc atg cct gcc	336
Phe Gln Leu Gln Glu Val Met Met Glu Phe Arg Gly Pro Met Pro Ala	
100 105 110	
ggc atg ctg att gag cgc tcc tca gac ttc ggt aag acc tgg cga gtg	384
Gly Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg Val	
115 120 125	
tac cag tac ctg gct gcc gac tgc acc tcc acc ttc cct cgg gtc cgc	432
Tyr Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val Arg	
130 135 140	
cag ggt cgg cct cag agc tgg cag gat gtt cgg tgc cag tcc ctg cct	480
Gln Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu Pro	
145 150 155 160	
cag agg cct aat gca cgc cta aat ggg ggg aag gtc caa ctt aac ctt	528
Gln Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn Leu	
165 170 175	
atg gat tta gtg tct ggg att cca gca act caa agt caa aaa att caa	576
Met Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile Gln	
180 185 190	
gag gtg ggg gag atc aca aac ttg aga gtc aat ttc acc agg ctg gcc	624
Glu Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu Ala	
195 200 205	
cct gtg ccc caa agg ggc tac cac cct ccc agc gcc tac tat gct gtg	672
Pro Val Pro Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala Val	
210 215 220	
tcc cag ctg cgt ctg cag ggg agc tgc ttc tgt cac ggc cat gct gat	720
Ser Gln Leu Arg Leu Gln Gly Ser Cys Phe Cys His Gly His Ala Asp	
225 230 235 240	
cgc tgc gca ccc aag cct ggg gcc tct gca ggc tcc acc gct gtg cag	768
Arg Cys Ala Pro Lys Pro Gly Ala Ser Ala Gly Ser Thr Ala Val Gln	
245 250 255	
gtc cac gat gtc tgc gtc tgc cag cac aac act gcc ggc cca aat tgt	816
Val His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro Asn Cys	
260 265 270	
gag cgc tgt gca ccc ttc tac aac aac cgg ccc tgg aga ccg gcg gag	864
Glu Arg Cys Ala Pro Phe Tyr Asn Asn Arg Pro Trp Arg Pro Ala Glu	
275 280 285	
ggc cag gac gcc cat gaa tgc caa agg tgc gac tgc aat ggg cac tca	912
Gly Gln Asp Ala His Glu Cys Gln Arg Cys Asp Cys Asn Gly His Ser	
290 295 300	
gag aca tgt cac ttt gac ccc gct gtg ttt gcc gcc agc cag ggg gca	960
Glu Thr Cys His Phe Asp Pro Ala Val Phe Ala Ala Ser Gln Gly Ala	
305 310 315 320	

tat gga ggt gtg tgt gac aat tgc cgg gac cac acc gaa ggc aag aac	1008
Tyr Gly Gly Val Cys Asp Asn Cys Arg Asp His Thr Glu Gly Lys Asn	
325 330 335	
tgt gag cgg tgt cag ctg cac tat ttc cgg aac cgg cgc ccg gga gct	1056
Cys Glu Arg Cys Gln Leu His Tyr Phe Arg Asn Arg Arg Pro Gly Ala	
340 345 350	
tcc att cag gag acc tgc atc tcc tgc gag tgt gat ccg gat ggg gca	1104
Ser Ile Gln Glu Thr Cys Ile Ser Cys Glu Cys Asp Pro Asp Gly Ala	
355 360 365	
gtc gca ggg gct ccc tgt gac cca gtg acc ggg cag tgt gtg tgc aag	1152
Val Ala Gly Ala Pro Cys Asp Pro Val Thr Gly Gln Cys Val Cys Lys	
370 375 380	
gag cat gtg cag gga gag cgc tgt gac cta tgc aag ccg ggc ttc act	1200
Glu His Val Gln Gly Glu Arg Cys Asp Leu Cys Lys Pro Gly Phe Thr	
385 390 395 400	
gga ctc acc tac gcc aac ccg cga cgg tgc cac cgc tgt gac tgc aac	1248
Gly Leu Thr Tyr Ala Asn Pro Arg Arg Cys His Arg Cys Asp Cys Asn	
405 410 415	
atc ctg ggg tcc cgg gag atg ccg tgt gac gag gag agt ggg cgc tgc	1296
Ile Leu Gly Ser Arg Glu Met Pro Cys Asp Glu Glu Ser Gly Arg Cys	
420 425 430	
ctt tgt ctg ccc aac gtg gtg ggt ccc aaa tgt gac cag tgt gct ccc	1344
Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln Cys Ala Pro	
435 440 445	
tac cac tgg aag ctg gcc agt ggc cag ggc tgt gaa ccg tgt gcc tgc	1392
Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys Ala Cys	
450 455 460	
gac ccg cac aac tcc ctc agc cca cag tgc aac cag ttc aca ggg cag	1440
Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn Gln Phe Thr Gly Gln	
465 470 475 480	
tgc ccc tgt cgg gaa ggc ttt ggt ggc ctg atg tgc agc gct gca gcc	1488
Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met Cys Ser Ala Ala Ala	
485 490 495	
atc cgc cag tgt cca gac cgg acc tat gga gac gtg gcc aca gga tgc	1536
Ile Arg Gln Cys Pro Asp Arg Thr Tyr Gly Asp Val Ala Thr Gly Cys	
500 505 510	
cga gcc tgt gac tgt gat ttc cgg gga aca gag ggc ccg ggc tgc gac	1584
Arg Ala Cys Asp Cys Asp Phe Arg Gly Thr Glu Gly Pro Gly Cys Asp	
515 520 525	
aag gca tca ggc cgc tgc ctc tgc cgc cct ggc ttg acc ggg ccc cgc	1632
Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly Leu Thr Gly Pro Arg	
530 535 540	
tgt gac cag tgc cag cga ggc tac tgc aat cgc tac ccg gtg tgc gtg	1680
Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg Tyr Pro Val Cys Val	
545 550 555 560	
gcc tgc cac cct tgc ttc cag acc tat gat gcg gac ctc cgg gag cag	1728

Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu Arg Glu Gln	
565 570 575	
gcc ctg cgc ttt ggt aga ctc ccg aat gcc acc gcc agc ctg tgg tca	1776
Ala Leu Arg Phe Gly Arg Leu Pro Asn Ala Thr Ala Ser Leu Trp Ser	
580 585 590	
ggg cct ggg ctg gag gac cgt ggc ctg gcc tcc cgg atc cta gat gca	1824
Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile Leu Asp Ala	
595 600 605	
aag agt aag att gag cag atc cga gca gtt ctc agc agc ccc gca gtc	1872
Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser Pro Ala Val	
610 615 620	
aca gag cag gag gtg gct cag gtg gcc agt gcc atc ctc tcc ctc agg	1920
Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu Ser Leu Arg	
625 630 635 640	
cga act ctc cag ggc ctg cag ctg gat ctg ccc ctg gag gag gag acg	1968
Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu Glu Thr	
645 650 655	
ttg tcc ctt ccg aga gac ctg gag agt ctt gac aga agc ttc aat ggt	2016
Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe Asn Gly	
660 665 670	
ctc ctt act atg tat cag agg aag agg gag cag ttt gaa aaa ata agc	2064
Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys Ile Ser	
675 680 685	
agt gct gat cct tca gga gcc ttc cgg atg ctg agc aca gcc tac gag	2112
Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu Ser Thr Ala Tyr Glu	
690 695 700	
cag tca gcc cag gct gct cag cag gtc tcc gac agc tcg cgc ctt ttg	2160
Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser Arg Leu Leu	
705 710 715 720	
gac cag ctc agg gac agc cgg aga gag gca gag agg ctg gtg cgg cag	2208
Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu Val Arg Gln	
725 730 735	
gcg gga gga gga gga ggc acc ggc agc ccc aag ctt gtg gcc ctg agg	2256
Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val Ala Leu Arg	
740 745 750	
ttg gag atg tct tcg ttg cct gac ctg aca ccc acc ttc aac aag ctc	2304
Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe Asn Lys Leu	
755 760 765	
tgt ggc aac tcc agg cag atg gct tgc acc cca ata tca tgc cct ggt	2352
Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser Cys Pro Gly	
770 775 780	
gag cta tgt ccc caa gac aat ggc aca gcc tgt gcg tcc cgc tgc agg	2400
Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys Ala Ser Arg Cys Arg	
785 790 795 800	
ggg gtc ctt ccc agg gcc ggt ggg gcc ttc ttg atg gcg ggg cag gtg	2448
Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu Met Ala Gly Gln Val	

805										810					815					
gct	gag	cag	ctg	cgg	ggc	ttc	aat	gcc	cag	ctc	cag	cgg	acc	agg	cag	2496				
Ala	Glu	Gln	Leu	Arg	Gly	Phe	Asn	Ala	Gln	Leu	Gln	Arg	Thr	Arg	Gln					
820					825					830										
atg	att	agg	gca	gcc	gag	gaa	tct	gcc	tca	cag	att	caa	tcc	agc	gcc	2544				
Met	Ile	Arg	Ala	Ala	Glu	Glu	Ser	Ala	Ser	Gln	Ile	Gln	Ser	Ser	Ala					
835					840					845										
cag	cgc	ttg	gag	acc	cag	gtg	agc	gcc	agc	cgc	tcc	cag	atg	gag	gaa	2592				
Gln	Arg	Leu	Glu	Thr	Gln	Val	Ser	Ala	Ser	Arg	Ser	Gln	Met	Glu	Glu					
850					855					860										
gat	gtc	aga	cgc	aca	cgg	ctc	cta	atc	cag	cag	gtc	cgg	gac	ttc	cta	2640				
Asp	Val	Arg	Arg	Thr	Arg	Leu	Leu	Ile	Gln	Gln	Val	Arg	Asp	Phe	Leu					
865					870					875					880					
aca	gac	ccc	gac	act	gat	gca	gcc	act	atc	cag	gag	gtc	agc	gag	gcc	2688				
Thr	Asp	Pro	Asp	Thr	Asp	Ala	Ala	Thr	Ile	Gln	Glu	Val	Ser	Glu	Ala					
885					890					895										
gtg	ctg	gcc	ctg	tgg	ctg	ccc	aca	gac	tca	gct	act	gtt	ctg	cag	aag	2736				
Val	Leu	Ala	Leu	Trp	Leu	Pro	Thr	Asp	Ser	Ala	Thr	Val	Leu	Gln	Lys					
900					905					910										
atg	aat	gag	atc	cag	gcc	att	gca	gcc	agg	ctc	ccc	aac	gtg	gac	ttg	2784				
Met	Asn	Glu	Ile	Gln	Ala	Ile	Ala	Ala	Arg	Leu	Pro	Asn	Val	Asp	Leu					
915					920					925										
gtg	ctg	tcc	cag	acc	aag	cag	gac	att	gcg	cgt	gcc	cgc	cgg	ttg	cag	2832				
Val	Leu	Ser	Gln	Thr	Lys	Gln	Asp	Ile	Ala	Arg	Ala	Arg	Arg	Leu	Gln					
930					935					940										
gct	gag	gct	gag	gaa	gcc	agg	agc	cga	gcc	cat	gca	gtg	gag	ggc	cag	2880				
Ala	Glu	Ala	Glu	Glu	Ala	Arg	Ser	Arg	Ala	His	Ala	Val	Glu	Gly	Gln					
945					950					955					960					
gtg	gag	gat	gtg	gtt	ggg	aac	ctg	cgg	cag	ggg	aca	gtg	gca	ctg	cag	2928				
Val	Glu	Asp	Val	Val	Gly	Asn	Leu	Arg	Gln	Gly	Thr	Val	Ala	Leu	Gln					
965					970					975										
gaa	gct	cag	gac	acc	atg	caa	ggc	acc	agc	cgg	tcc	ctt	cgg	ctt	atc	2976				
Glu	Ala	Gln	Asp	Thr	Met	Gln	Gly	Thr	Ser	Arg	Ser	Leu	Arg	Leu	Ile					
980					985					990										
cag	gac	agg	gtt	gct	gag	gtt	cag	cag	gta	ctg	cgg	cca	gca	gaa	aag	3024				
Gln	Asp	Arg	Val	Ala	Glu	Val	Gln	Gln	Val	Leu	Arg	Pro	Ala	Glu	Lys					
995					1000					1005										
ctg	gtg	aca	agc	atg	acc	aag	cag	ctg	ggt	gac	ttc	tgg	aca	cgg	atg	3072				
Leu	Val	Thr	Ser	Met	Thr	Lys	Gln	Leu	Gly	Asp	Phe	Trp	Thr	Arg	Met					
1010					1015					1020										
gag	gag	ctc	cgc	cac	caa	gcc	cgg	cag	cag	ggg	gca	gag	gca	gtc	cag	3120				
Glu	Glu	Leu	Arg	His	Gln	Ala	Arg	Gln	Gln	Gly	Ala	Glu	Ala	Val	Gln					
1025					1030					1035					1040					
gcc	cag	cag	ctt	gcg	gaa	ggt	gcc	agc	gag	cag	gca	ttg	agt	gcc	caa	3168				
Ala	Gln	Gln	Leu	Ala	Glu	Gly	Ala	Ser	Glu	Gln	Ala	Leu	Ser	Ala	Gln					
1045					1050					1055										

gag gga ttt gag aga ata aaa caa aag tat gct gag ttg aag gac cgg 3216
 Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys Asp Arg
 1060 1065 1070

ttg ggt cag agt tcc atg ctg ggt gag cag ggt gcc cgg atc cag agt 3264
 Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg Ile Gln Ser
 1075 1080 1085

gtg aag aca gag gca gag gag ctg ttt ggg gag acc atg gag atg atg 3312
 Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu Thr Met Glu Met Met
 1090 1095 1100

gac agg atg aaa gac atg gag ttg gag ctg ctg cgg ggc agc cag gcc 3360
 Asp Arg Met Lys Asp Met Glu Leu Glu Leu Arg Gly Ser Gln Ala
 1105 1110 1115 1120

atc atg ctg cgc tca gcg gac ctg aca gga ctg gag aag cgt gtg gag 3408
 Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu Glu Lys Arg Val Glu
 1125 1130 1135

cag atc cgt gac cac atc aat ggg cgc gtg ctc tac tat gcc acc tgc 3456
 Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu Tyr Tyr Ala Thr Cys
 1140 1145 1150

aag tgatgctaca cggtccagcc cggtgccccca ctcatctgcg cgctttgctt 3509
 Lys

ttggttgggg ggcagattgg gttggaatgc tttccatctc caggagactt tcatgtagcc 3569

caaagtacag cctggaccac ccctgggtgtg tgtagctagt aagattaccc tgagctgcag 3629

ctgagcctga gccaatggga cagttacact tgacagacaa agatgggtgga gattggcatg 3689

ccattgaaac taagagctct caagtcaagg aagctgggct gggcagtatc ccccgctttt 3749

agttctccac 3759

<210> 16
 <211> 1153
 <212> PRT
 <213> Homo sapiens

<400> 16
 Gln Gln Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu
 1 5 10 15

Leu Val Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu
 20 25 30

Thr Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys
 35 40 45

Cys Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His Arg
 50 55 60

Val Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln Ser
 65 70 75 80

Gln Asn Asp Val Asn Pro Val S r Leu Gln Leu Asp Leu Asp Arg Arg

85										90					95						
Phe	Gln	Leu	Gln	Glu	Val	Met	Met	Glu	Phe	Arg	Gly	Pro	Met	Pro	Ala						
			100					105					110								
Gly	Met	Leu	Ile	Glu	Arg	Ser	Ser	Asp	Phe	Gly	Lys	Thr	Trp	Arg	Val						
		115					120					125									
Tyr	Gln	Tyr	Leu	Ala	Ala	Asp	Cys	Thr	Ser	Thr	Phe	Pro	Arg	Val	Arg						
		130				135					140										
Gln	Gly	Arg	Pro	Gln	Ser	Trp	Gln	Asp	Val	Arg	Cys	Gln	Ser	Leu	Pro						
145					150					155					160						
Gln	Arg	Pro	Asn	Ala	Arg	Leu	Asn	Gly	Gly	Lys	Val	Gln	Leu	Asn	Leu						
				165					170					175							
Met	Asp	Leu	Val	Ser	Gly	Ile	Pro	Ala	Thr	Gln	Ser	Gln	Lys	Ile	Gln						
			180					185					190								
Glu	Val	Gly	Glu	Ile	Thr	Asn	Leu	Arg	Val	Asn	Phe	Thr	Arg	Leu	Ala						
		195					200					205									
Pro	Val	Pro	Gln	Arg	Gly	Tyr	His	Pro	Pro	Ser	Ala	Tyr	Tyr	Ala	Val						
		210				215					220										
Ser	Gln	Leu	Arg	Leu	Gln	Gly	Ser	Cys	Phe	Cys	His	Gly	His	Ala	Asp						
225					230					235					240						
Arg	Cys	Ala	Pro	Lys	Pro	Gly	Ala	Ser	Ala	Gly	Ser	Thr	Ala	Val	Gln						
				245					250					255							
Val	His	Asp	Val	Cys	Val	Cys	Gln	His	Asn	Thr	Ala	Gly	Pro	Asn	Cys						
			260					265					270								
Glu	Arg	Cys	Ala	Pro	Phe	Tyr	Asn	Asn	Arg	Pro	Trp	Arg	Pro	Ala	Glu						
		275					280					285									
Gly	Gln	Asp	Ala	His	Glu	Cys	Gln	Arg	Cys	Asp	Cys	Asn	Gly	His	Ser						
		290				295					300										
Glu	Thr	Cys	His	Phe	Asp	Pro	Ala	Val	Phe	Ala	Ala	Ser	Gln	Gly	Ala						
305					310					315					320						
Tyr	Gly	Gly	Val	Cys	Asp	Asn	Cys	Arg	Asp	His	Thr	Glu	Gly	Lys	Asn						
				325					330					335							
Cys	Glu	Arg	Cys	Gln	Leu	His	Tyr	Phe	Arg	Asn	Arg	Arg	Pro	Gly	Ala						
			340					345					350								
Ser	Ile	Gln	Glu	Thr	Cys	Ile	Ser	Cys	Glu	Cys	Asp	Pro	Asp	Gly	Ala						
			355				360					365									
Val	Ala	Gly	Ala	Pro	Cys	Asp	Pro	Val	Thr	Gly	Gln	Cys	Val	Cys	Lys						
			370			375					380										
Glu	His	Val	Gln	Gly	Glu	Arg	Cys	Asp	Leu	Cys	Lys	Pro	Gly	Phe	Thr						
385					390					395					400						
Gly	L u	Thr	Tyr	Ala	Asn	Pro	Arg	Arg	Cys	His	Arg	Cys	Asp	Cys	Asn						
				405					410					415							

Ile Leu Gly Ser Arg Glu Met Pro Cys Asp Glu Glu Ser Gly Arg Cys
420 425 430

Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln Cys Ala Pro
435 440 445

Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys Ala Cys
450 455 460

Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn Gln Phe Thr Gly Gln
465 470 475 480

Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met Cys Ser Ala Ala Ala
485 490 495

Ile Arg Gln Cys Pro Asp Arg Thr Tyr Gly Asp Val Ala Thr Gly Cys
500 505 510

Arg Ala Cys Asp Cys Asp Phe Arg Gly Thr Glu Gly Pro Gly Cys Asp
515 520 525

Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly Leu Thr Gly Pro Arg
530 535 540

Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg Tyr Pro Val Cys Val
545 550 555 560

Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu Arg Glu Gln
565 570 575

Ala Leu Arg Phe Gly Arg Leu Pro Asn Ala Thr Ala Ser Leu Trp Ser
580 585 590

Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile Leu Asp Ala
595 600 605

Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser Pro Ala Val
610 615 620

Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu Ser Leu Arg
625 630 635 640

Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu Glu Thr
645 650 655

Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe Asn Gly
660 665 670

Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys Ile Ser
675 680 685

Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu Ser Thr Ala Tyr Glu
690 695 700

Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser Arg Leu Leu
705 710 715 720

Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu Val Arg Gln
725 730 735

Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val Ala Leu Arg
740 745 750

Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe Asn Lys Leu
755 760 765

Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser Cys Pro Gly
770 775 780

Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys Ala Ser Arg Cys Arg
785 790 795 800

Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu Met Ala Gly Gln Val
805 810 815

Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr Arg Gln
820 825 830

Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser Ser Ala
835 840 845

Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg Ser Gln Met Glu Glu
850 855 860

Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln Val Arg Asp Phe Leu
865 870 875 880

Thr Asp Pro Asp Thr Asp Ala Ala Thr Ile Gln Glu Val Ser Glu Ala
885 890 895

Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala Thr Val Leu Gln Lys
900 905 910

Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu Pro Asn Val Asp Leu
915 920 925

Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg Leu Gln
930 935 940

Ala Glu Ala Glu Glu Ala Arg Ser Arg Ala His Ala Val Glu Gly Gln
945 950 955 960

Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val Ala Leu Gln
965 970 975

Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu Arg Leu Ile
980 985 990

Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro Ala Glu Lys
995 1000 1005

Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp Thr Arg Met
1010 1015 1020

Glu Glu Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu Ala Val Gln
1025 1030 1035 1040

Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln Ala Leu Ser Ala Gln
1045 1050 1055

Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys Asp Arg

1060	1065	1070
Leu Gly Gln Ser Ser Met	Leu Gly Glu Gln Gly Ala Arg	Ile Gln Ser
1075	1080	1085
Val Lys Thr Glu Ala Glu Glu	Leu Phe Gly Glu Thr Met	Glu Met Met
1090	1095	1100
Asp Arg Met Lys Asp Met	Glu Leu Glu Leu Arg Gly	Ser Gln Ala
1105	1110	1120
Ile Met Leu Arg Ser Ala Asp	Leu Thr Gly Leu Glu Lys	Arg Val Glu
1125	1130	1135
Gln Ile Arg Asp His Ile Asn	Gly Arg Val Leu Tyr Tyr	Ala Thr Cys
1140	1145	1150

Lys

<210> 17
 <211> 3621
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(3617)

<220>
 <221> sig_peptide
 <222> (60)..(110)

<220>
 <221> misc_feature
 <222> (123)..(146)

<400> 17
 gtttaaactt aagcttctgc ctgccgcctg cctgcctgcc actgagggtt cccagcacc 59

atg agg gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gct ctg	107
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu	
1 5 10 15	
gca gcc cca cta gcc gac tac aag gac gac gat gac aag cta gcc caa	155
Ala Ala Pro Leu Ala Asp Tyr Lys Asp Asp Asp Lys Leu Ala Gln	
20 25 30	
caa gcc tgc tcc cgt ggg gcc tgc tat cca cct gtt ggg gac ctg ctt	203
Gln Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu Leu	
35 40 45	
gtt ggg agg acc cgg ttt ctc cga gct tca tct acc tgt gga ctg acc	251
Val Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu Thr	
50 55 60	
aag cct gag acc tac tgc acc cag tat ggc gag tgg cag atg aaa tgc	299
Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys Cys	
65 70 75 80	

tgc aag tgt gac tcc agg cag cct cac aac tac tac agt cac cga gta	347
Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His Arg Val	
85 90 95	
gag aat gtg gct tca tcc tcc ggc ccc atg cgc tgg tgg cag tcc cag	395
Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln Ser Gln	
100 105 110	
aat gat gtg aac cct gtc tct ctg cag ctg gac ctg gac agg aga ttc	443
Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg Arg Phe	
115 120 125	
cag ctt caa gaa gtc atg atg gag ttc cag ggg ccc atg cct gcc ggc	491
Gln Leu Gln Glu Val Met Met Glu Phe Gln Gly Pro Met Pro Ala Gly	
130 135 140	
atg ctg att gag cgc tcc tca gac ttc ggt aag acc tgg cga gtg tac	539
Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg Val Tyr	
145 150 155 160	
cag tac ctg gct gcc gac tgc acc tcc acc ttc cct cgg gtc cgc cag	587
Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val Arg Gln	
165 170 175	
ggt cgg cct cag agc tgg cag gat gtt cgg tgc cag tcc ctg cct cag	635
Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu Pro Gln	
180 185 190	
agg cct aat gca cgc cta aat ggg ggg aag gtc caa ctt aac ctt atg	683
Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn Leu Met	
195 200 205	
gat tta gtg tct ggg att cca gca act caa agt caa aaa att caa gag	731
Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile Gln Glu	
210 215 220	
gtg ggg gag atc aca aac ttg aga gtc aat ttc acc agg ctg gcc cct	779
Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu Ala Pro	
225 230 235 240	
gtg ccc caa agg ggc tac cac cct ccc agc gcc tac tat gct gtg tcc	827
Val Pro Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala Val Ser	
245 250 255	
cag ctc cgt ctg cag ggg agc tgc ttc tgt cac ggc cat gct gat cgc	875
Gln Leu Arg Leu Gln Gly Ser Cys Phe Cys His Gly His Ala Asp Arg	
260 265 270	
tgc gca ccc aag cct ggg gcc tct gca ggc ccc tcc acc gct gtg cag	923
Cys Ala Pro Lys Pro Gly Ala Ser Ala Gly Pro Ser Thr Ala Val Gln	
275 280 285	
gtc cac gat gtc tgc gtc tgc cag cac aac act gcc ggc cca aat tgt	971
Val His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro Asn Cys	
290 295 300	
gag cgc tgt gca ccc ttc tac aac aac cgg ccc tgg aga ccg gcg gag	1019
Glu Arg Cys Ala Pro Ph Tyr Asn Asn Arg Pro Trp Arg Pro Ala Glu	
305 310 315 320	
ggc cag gac gcc cat gaa tgc caa agg tgc gac tgc aat ggg cac tca	1067

Gly	Gln	Asp	Ala	His	Glu	Cys	Gln	Arg	Cys	Asp	Cys	Asn	Gly	His	Ser		
				325					330					335			
gag	aca	tgt	cac	ttt	gac	ccc	gct	gtg	ttt	gcc	gcc	agc	cag	ggg	gca	1115	
Glu	Thr	Cys	His	Phe	Asp	Pro	Ala	Val	Phe	Ala	Ala	Ser	Gln	Gly	Ala		
			340					345					350				
tat	gga	ggt	gtg	tgt	gac	aat	tgc	cgg	gac	cac	acc	gaa	ggc	aag	aac	1163	
Tyr	Gly	Gly	Val	Cys	Asp	Asn	Cys	Arg	Asp	His	Thr	Glu	Gly	Lys	Asn		
		355					360					365					
tgt	gag	cgg	tgt	cag	ctg	cac	tat	ttc	cgg	aac	cgg	cgc	ccg	gga	gct	1211	
Cys	Glu	Arg	Cys	Gln	Leu	His	Tyr	Phe	Arg	Asn	Arg	Arg	Pro	Gly	Ala		
	370					375					380						
tcc	att	cag	gag	acc	tgc	atc	tcc	tgc	gag	tgt	gat	ccg	gat	ggg	gca	1259	
Ser	Ile	Gln	Glu	Thr	Cys	Ile	Ser	Cys	Glu	Cys	Asp	Pro	Asp	Gly	Ala		
385					390				395					400			
gtg	cca	ggg	gct	ccc	tgt	gac	cca	gtg	acc	ggg	cag	tgt	gtg	tgc	aag	1307	
Val	Pro	Gly	Ala	Pro	Cys	Asp	Pro	Val	Thr	Gly	Gln	Cys	Val	Cys	Lys		
			405					410					415				
gag	cat	gtg	cag	gga	gag	cgc	tgt	gac	cta	tgc	aag	ccg	ggc	ttc	act	1355	
Glu	His	Val	Gln	Gly	Glu	Arg	Cys	Asp	Leu	Cys	Lys	Pro	Gly	Phe	Thr		
			420				425					430					
gga	ctc	acc	tac	gcc	aac	ccg	cag	ggc	tgc	cac	cgc	tgt	gac	tgc	aac	1403	
Gly	Leu	Thr	Tyr	Ala	Asn	Pro	Gln	Gly	Cys	His	Arg	Cys	Asp	Cys	Asn		
		435					440					445					
atc	ctg	ggg	tcc	cgg	agg	gac	atg	ccg	tgt	gac	gag	gag	agt	ggg	cgc	1451	
Ile	Leu	Gly	Ser	Arg	Arg	Asp	Met	Pro	Cys	Asp	Glu	Glu	Ser	Gly	Arg		
	450					455					460						
tgc	ctt	tgt	ctg	ccc	aac	gtg	gtg	ggt	ccc	aaa	tgt	gac	cag	tgt	gct	1499	
Cys	Leu	Cys	Leu	Pro	Asn	Val	Val	Gly	Pro	Lys	Cys	Asp	Gln	Cys	Ala		
465					470					475					480		
ccc	tac	cac	tgg	aag	ctg	gcc	agt	ggc	cag	ggc	tgt	gaa	ccg	tgt	gcc	1547	
Pro	Tyr	His	Trp	Lys	Leu	Ala	Ser	Gly	Gln	Gly	Cys	Glu	Pro	Cys	Ala		
			485					490				495					
tgc	gac	ccg	cac	aac	tcc	ctc	agc	cca	cag	tgc	aac	cag	ttc	aca	ggg	1595	
Cys	Asp	Pro	His	Asn	Ser	Leu	Ser	Pro	Gln	Cys	Asn	Gln	Phe	Thr	Gly		
			500					505				510					
cag	tgc	ccc	tgt	cgg	gaa	ggc	ttt	ggt	ggc	ctg	atg	tgc	agc	gct	gca	1643	
Gln	Cys	Pro	Cys	Arg	Glu	Gly	Phe	Gly	Gly	Leu	Met	Cys	Ser	Ala	Ala		
		515				520						525					
gcc	atc	cgc	cag	tgt	cca	gac	cgg	acc	tat	gga	gac	gtg	gcc	aca	gga	1691	
Ala	Ile	Arg	Gln	Cys	Pro	Asp	Arg	Thr	Tyr	Gly	Asp	Val	Ala	Thr	Gly		
	530					535					540						
tgc	cga	gcc	tgt	gac	tgt	gat	ttc	cgg	gga	aca	gag	ggc	ccg	ggc	tgc	1739	
Cys	Arg	Ala	Cys	Asp	Cys	Asp	Phe	Arg	Gly	Thr	Glu	Gly	Pro	Gly	Cys		
545					550					555					560		
gac	aag	gca	tca	ggc	cgc	tgc	ctc	tgc	cgc	cct	ggc	ttg	acc	ggg	ccc	1787	
Asp	Lys	Ala	Ser	Gly	Arg	Cys	Leu	Cys	Arg	Pro	Gly	Leu	Thr	Gly	Pro		

ggt gag cta tgt ccc caa gac aat ggc aca gcc tgt ggc tcc cgc tgc	2555
Gly Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys Gly Ser Arg Cys	
820 825 830	
agg ggt gtc ctt ccc agg gcc ggt ggg gcc ttc ttg atg gcg ggg cag	2603
Arg Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu Met Ala Gly Gln	
835 840 845	
gtg gct gag cag ctg cgg ggc ttc aat gcc cag ctc cag cgg acc agg	2651
Val Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr Arg	
850 855 860	
cag atg att agg gca gcc gag gaa tct gcc tca cag att caa tcc agt	2699
Gln Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser Ser	
865 870 875 880	
gcc cag cgc ttg gag acc cag gtg agc gcc agc cgc tcc cag atg gag	2747
Ala Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg Ser Gln Met Glu	
885 890 895	
gaa gat gtc aga cgc aca cgg ctc cta atc cag cag gtc cgg gac ttc	2795
Glu Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln Val Arg Asp Phe	
900 905 910	
cta aca gac ccc gac act gat gca gcc act atc cag gag gtc agc gag	2843
Leu Thr Asp Pro Asp Thr Asp Ala Ala Thr Ile Gln Glu Val Ser Glu	
915 920 925	
gcc gtg ctg gcc ctg tgg ctg ccc aca gac tca gct act gtt ctg cag	2891
Ala Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala Thr Val Leu Gln	
930 935 940	
aag atg aat gag atc cag gcc att gca gcc agg ctc ccc aac gtg gac	2939
Lys Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu Pro Asn Val Asp	
945 950 955 960	
ttg gtg ctg tcc cag acc aag cag gac att gcg cgt gcc cgc cgg ttg	2987
Leu Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg Leu	
965 970 975	
cag gct gag gct gag gaa gcc agg agc cga gcc cat gca gtg gag ggc	3035
Gln Ala Glu Ala Glu Glu Ala Arg Ser Arg Ala His Ala Val Glu Gly	
980 985 990	
cag gtg gaa gat gtg gtt ggg aac ctg cgg cag ggg aca gtg gca ctg	3083
Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val Ala Leu	
995 1000 1005	
cag gaa gct cag gac acc atg caa ggc acc agc cgc tcc ctt cgg ctt	3131
Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu Arg Leu	
1010 1015 1020	
atc cag gac agg gtt gct gag gtt cag cag gta ctg cgg cca gca gaa	3179
Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro Ala Glu	
1025 1030 1035 1040	
aag ctg gtg aca agc atg acc aag cag ctg ggt gac ttc tgg aca cgg	3227
Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp Thr Arg	
1045 1050 1055	

atg gag gag ctc cgc cac caa gcc cgg cag cag ggg gca gag gca gtc 3275
 Met Glu Glu Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu Ala Val
 1060 1065 1070

cag gcc cag cag ctt gcg gaa ggt gcc agc gag cag gca ttg agt gcc 3323
 Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln Ala Leu Ser Ala
 1075 1080 1085

caa gag gga ttt gag aga ata aaa caa aag tat gct gag ttg aag gac 3371
 Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys Asp
 1090 1095 1100

cgg ttg ggt cag agt tcc atg ctg ggt gag cag ggt gcc cgg atc cag 3419
 Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg Ile Gln
 1105 1110 1115 1120

agt gtg aag aca gag gca gag gag ctg ttt ggg gag acc atg gag atg 3467
 Ser Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu Thr Met Glu Met
 1125 1130 1135

atg gac agg atg aaa gac atg gag ttg gag ctg ctg cgg ggc agc cag 3515
 Met Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu Arg Gly Ser Gln
 1140 1145 1150

gcc atc atg ctg cgc tca gcg gac ctg aca gga ctg gag aag cgt gtg 3563
 Ala Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu Glu Lys Arg Val
 1155 1160 1165

gag cag atc cgt gac cac atc aat ggg cgc gtg ctc tac tat gcc acc 3611
 Glu Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu Tyr Tyr Ala Thr
 1170 1175 1180

tgc aag tgat 3621
 Cys Lys
 1185

<210> 18
 <211> 1186
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 1 5 10 15

Ala Ala Pro Leu Ala Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala Gln
 20 25 30

Gln Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu Leu
 35 40 45

Val Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu Thr
 50 55 60

Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys Cys
 65 70 75 80

Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His Arg Val
 85 90 95

Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln Ser Gln
100 105 110

Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg Arg Phe
115 120 125

Gln Leu Gln Glu Val Met Met Glu Phe Gln Gly Pro Met Pro Ala Gly
130 135 140

Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg Val Tyr
145 150 155 160

Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val Arg Gln
165 170 175

Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu Pro Gln
180 185 190

Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn Leu Met
195 200 205

Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile Gln Glu
210 215 220

Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu Ala Pro
225 230 235 240

Val Pro Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala Val Ser
245 250 255

Gln Leu Arg Leu Gln Gly Ser Cys Phe Cys His Gly His Ala Asp Arg
260 265 270

Cys Ala Pro Lys Pro Gly Ala Ser Ala Gly Pro Ser Thr Ala Val Gln
275 280 285

Val His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro Asn Cys
290 295 300

Glu Arg Cys Ala Pro Phe Tyr Asn Asn Arg Pro Trp Arg Pro Ala Glu
305 310 315 320

Gly Gln Asp Ala His Glu Cys Gln Arg Cys Asp Cys Asn Gly His Ser
325 330 335

Glu Thr Cys His Phe Asp Pro Ala Val Phe Ala Ala Ser Gln Gly Ala
340 345 350

Tyr Gly Gly Val Cys Asp Asn Cys Arg Asp His Thr Glu Gly Lys Asn
355 360 365

Cys Glu Arg Cys Gln Leu His Tyr Phe Arg Asn Arg Arg Pro Gly Ala
370 375 380

Ser Ile Gln Glu Thr Cys Ile Ser Cys Glu Cys Asp Pro Asp Gly Ala
385 390 395 400

Val Pro Gly Ala Pro Cys Asp Pro Val Thr Gly Gln Cys Val Cys Lys
405 410 415

Glu His Val Gln Gly Glu Arg Cys Asp Leu Cys Lys Pro Gly Phe Thr

420					425					430						
Gly	Leu	Thr	Tyr	Ala	Asn	Pro	Gln	Gly	Cys	His	Arg	Cys	Asp	Cys	Asn	
435					440					445						
Ile	Leu	Gly	Ser	Arg	Arg	Asp	Met	Pro	Cys	Asp	Glu	Glu	Ser	Gly	Arg	
450					455					460						
Cys	Leu	Cys	Leu	Pro	Asn	Val	Val	Gly	Pro	Lys	Cys	Asp	Gln	Cys	Ala	
465					470					475					480	
Pro	Tyr	His	Trp	Lys	Leu	Ala	Ser	Gly	Gln	Gly	Cys	Glu	Pro	Cys	Ala	
485					490					495						
Cys	Asp	Pro	His	Asn	Ser	Leu	Ser	Pro	Gln	Cys	Asn	Gln	Phe	Thr	Gly	
500					505					510						
Gln	Cys	Pro	Cys	Arg	Glu	Gly	Phe	Gly	Gly	Leu	Met	Cys	Ser	Ala	Ala	
515					520					525						
Ala	Ile	Arg	Gln	Cys	Pro	Asp	Arg	Thr	Tyr	Gly	Asp	Val	Ala	Thr	Gly	
530					535					540						
Cys	Arg	Ala	Cys	Asp	Cys	Asp	Phe	Arg	Gly	Thr	Glu	Gly	Pro	Gly	Cys	
545					550					555					560	
Asp	Lys	Ala	Ser	Gly	Arg	Cys	Leu	Cys	Arg	Pro	Gly	Leu	Thr	Gly	Pro	
565					570					575						
Arg	Cys	Asp	Gln	Cys	Gln	Arg	Gly	Tyr	Cys	Asn	Arg	Tyr	Pro	Val	Cys	
580					585					590						
Val	Ala	Cys	His	Pro	Cys	Phe	Gln	Thr	Tyr	Asp	Ala	Asp	Leu	Arg	Glu	
595					600					605						
Gln	Ala	Leu	Arg	Phe	Gly	Arg	Leu	Arg	Asn	Ala	Thr	Ala	Ser	Leu	Trp	
610					615					620						
Ser	Gly	Pro	Gly	Leu	Glu	Asp	Arg	Gly	Leu	Ala	Ser	Arg	Ile	Leu	Asp	
625					630					635					640	
Ala	Lys	Ser	Lys	Ile	Glu	Gln	Ile	Arg	Ala	Val	Leu	Ser	Ser	Pro	Ala	
645					650					655						
Val	Thr	Glu	Gln	Glu	Val	Ala	Gln	Val	Ala	Ser	Ala	Ile	Leu	Ser	Leu	
660					665					670						
Arg	Arg	Thr	Leu	Gln	Gly	Leu	Gln	Leu	Asp	Leu	Pro	Leu	Glu	Glu	Glu	
675					680					685						
Thr	Leu	Ser	Leu	Pro	Arg	Asp	Leu	Glu	Ser	Leu	Asp	Arg	Ser	Phe	Asn	
690					695					700						
Gly	Leu	Leu	Thr	Met	Tyr	Gln	Arg	Lys	Arg	Glu	Gln	Phe	Glu	Lys	Ile	
705					710					715					720	
Ser	Ser	Ala	Asp	Pro	Ser	Gly	Ala	Phe	Arg	Met	Leu	Ser	Thr	Ala	Tyr	
725					730					735						
Glu	Gln	Ser	Ala	Gln	Ala	Ala	Gln	Gln	Val	Ser	Asp	Ser	Ser	Arg	Leu	
740					745					750						

Leu Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu Val Arg
755 760 765

Gln Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val Ala Leu
770 775 780

Arg Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe Asn Lys
785 790 795 800

Leu Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser Cys Pro
805 810 815

Gly Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys Gly Ser Arg Cys
820 825 830

Arg Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu Met Ala Gly Gln
835 840 845

Val Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr Arg
850 855 860

Gln Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser Ser
865 870 875 880

Ala Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg Ser Gln Met Glu
885 890 895

Glu Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln Val Arg Asp Phe
900 905 910

Leu Thr Asp Pro Asp Thr Asp Ala Ala Thr Ile Gln Glu Val Ser Glu
915 920 925

Ala Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala Thr Val Leu Gln
930 935 940

Lys Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu Pro Asn Val Asp
945 950 955 960

Leu Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg Leu
965 970 975

Gln Ala Glu Ala Glu Glu Ala Arg Ser Arg Ala His Ala Val Glu Gly
980 985 990

Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val Ala Leu
995 1000 1005

Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu Arg Leu
1010 1015 1020

Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro Ala Glu
1025 1030 1035 1040

Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp Thr Arg
1045 1050 1055

M t Glu Glu Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu Ala Val
1060 1065 1070

Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln Ala Leu Ser Ala
 1075 1080 1085
 Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys Asp
 1090 1095 1100
 Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg Ile Gln
 1105 1110 1115 1120
 Ser Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu Thr Met Glu Met
 1125 1130 1135
 Met Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu Arg Gly Ser Gln
 1140 1145 1150
 Ala Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu Glu Lys Arg Val
 1155 1160 1165
 Glu Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu Tyr Tyr Ala Thr
 1170 1175 1180

Cys Lys
 1185

<210> 19
 <211> 3511
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (7)..(3507)

<220>
 <221> misc_feature
 <222> (13)..(36)

<400> 19
 gcccca cta gcc gac tac aag gac gac gat gac aag cta gcc caa caa 48
 Leu Ala Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala Gln Gln
 1 5 10
 gcc tgc tcc cgt ggg gcc tgc tat cca cct gtt ggg gac ctg ctt gtt 96
 Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu Leu Val
 15 20 25 30
 ggg agg acc cgg ttt ctc cga gct tca tct acc tgt gga ctg acc aag 144
 Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu Thr Lys
 35 40 45
 cct gag acc tac tgc acc cag tat ggc gag tgg cag atg aaa tgc tgc 192
 Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys Cys Cys
 50 55 60
 aag tgt gac tcc agg cag cct cac aac tac tac agt cac cga gta gag 240
 Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His Arg Val Glu
 65 70 75
 aat gtg gct tca tcc tcc ggc ccc atg cgc tgg tgg cag tcc cag aat 288
 Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln Ser Gln Asn

80	85	90	
gat gtg aac cct gtc tct ctg cag ctg gac ctg gac agg aga ttc cag Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg Arg Phe Gln 95 100 105 110			336
ctt caa gaa gtc atg atg gag ttc cag ggg ccc atg cct gcc ggc atg Leu Gln Glu Val Met Met Glu Phe Gln Gly Pro Met Pro Ala Gly Met 115 120 125			384
ctg att gag cgc tcc tca gac ttc ggt aag acc tgg cga gtg tac cag Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg Val Tyr Gln 130 135 140			432
tac ctg gct gcc gac tgc acc tcc acc ttc cct cgg gtc cgc cag ggt Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val Arg Gln Gly 145 150 155			480
cgg cct cag agc tgg cag gat gtt cgg tgc cag tcc ctg cct cag agg Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu Pro Gln Arg 160 165 170			528
cct aat gca cgc cta aat ggg ggg aag gtc caa ctt aac ctt atg gat Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn Leu Met Asp 175 180 185 190			576
tta gtg tct ggg att cca gca act caa agt caa aaa att caa gag gtg Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile Gln Glu Val 195 200 205			624
ggg gag atc aca aac ttg aga gtc aat ttc acc agg ctg gcc cct gtg Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu Ala Pro Val 210 215 220			672
ccc caa agg ggc tac cac cct ccc agc gcc tac tat gct gtg tcc cag Pro Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala Val Ser Gln 225 230 235			720
ctc cgt ctg cag ggg agc tgc ttc tgt cac ggc cat gct gat cgc tgc Leu Arg Leu Gln Gly Ser Cys Phe Cys His Gly His Ala Asp Arg Cys 240 245 250			768
gca ccc aag cct ggg gcc tct gca ggc ccc tcc acc gct gtg cag gtc Ala Pro Lys Pro Gly Ala Ser Ala Gly Pro Ser Thr Ala Val Gln Val 255 260 265 270			816
cac gat gtc tgc gtc tgc cag cac aac act gcc ggc cca aat tgt gag His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro Asn Cys Glu 275 280 285			864
cgc tgt gca ccc ttc tac aac aac cgg ccc tgg aga ccg gcg gag ggc Arg Cys Ala Pro Phe Tyr Asn Asn Arg Pro Trp Arg Pro Ala Glu Gly 290 295 300			912
cag gac gcc cat gaa tgc caa agg tgc gac tgc aat ggg cac tca gag Gln Asp Ala His Glu Cys Gln Arg Cys Asp Cys Asn Gly His Ser Glu 305 310 315			960
aca tgt cac ttt gac ccc gct gtg ttt gcc gcc agc cag ggg gca tat Thr Cys His Phe Asp Pro Ala Val Phe Ala Ala Ser Gln Gly Ala Tyr 320 325 330			1008

gga ggt gtg tgt gac aat tgc cgg gac cac acc gaa ggc aag aac tgt	1056
Gly Gly Val Cys Asp Asn Cys Arg Asp His Thr Glu Gly Lys Asn Cys	
335 340 345 350	
gag cgg tgt cag ctg cac tat ttc cgg aac cgg cgc ccg gga gct tcc	1104
Glu Arg Cys Gln Leu His Tyr Phe Arg Asn Arg Arg Pro Gly Ala Ser	
355 360 365	
att cag gag acc tgc atc tcc tgc gag tgt gat ccg gat ggg gca gtg	1152
Ile Gln Glu Thr Cys Ile Ser Cys Glu Cys Asp Pro Asp Gly Ala Val	
370 375 380	
cca ggg gct ccc tgt gac cca gtg acc ggg cag tgt gtg tgc aag gag	1200
Pro Gly Ala Pro Cys Asp Pro Val Thr Gly Gln Cys Val Cys Lys Glu	
385 390 395	
cat gtg cag gga gag cgc tgt gac cta tgc aag ccg ggc ttc act gga	1248
His Val Gln Gly Glu Arg Cys Asp Leu Cys Lys Pro Gly Phe Thr Gly	
400 405 410	
ctc acc tac gcc aac ccg cag ggc tgc cac cgc tgt gac tgc aac atc	1296
Leu Thr Tyr Ala Asn Pro Gln Gly Cys His Arg Cys Asp Cys Asn Ile	
415 420 425 430	
ctg ggg tcc cgg agg gac atg ccg tgt gac gag gag agt ggg cgc tgc	1344
Leu Gly Ser Arg Arg Asp Met Pro Cys Asp Glu Glu Ser Gly Arg Cys	
435 440 445	
ctt tgt ctg ccc aac gtg gtg ggt ccc aaa tgt gac cag tgt gct ccc	1392
Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln Cys Ala Pro	
450 455 460	
tac cac tgg aag ctg gcc agt ggc cag ggc tgt gaa ccg tgt gcc tgc	1440
Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys Ala Cys	
465 470 475	
gac ccg cac aac tcc ctc agc cca cag tgc aac cag ttc aca ggg cag	1488
Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn Gln Phe Thr Gly Gln	
480 485 490	
tgc ccc tgt cgg gaa ggc ttt ggt ggc ctg atg tgc agc gct gca gcc	1536
Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met Cys Ser Ala Ala Ala	
495 500 505 510	
atc cgc cag tgt cca gac cgg acc tat gga gac gtg gcc aca gga tgc	1584
Ile Arg Gln Cys Pro Asp Arg Thr Tyr Gly Asp Val Ala Thr Gly Cys	
515 520 525	
cga gcc tgt gac tgt gat ttc cgg gga aca gag ggc ccg ggc tgc gac	1632
Arg Ala Cys Asp Cys Asp Phe Arg Gly Thr Glu Gly Pro Gly Cys Asp	
530 535 540	
aag gca tca ggc cgc tgc ctc tgc cgc cct ggc ttg acc ggg ccc cgc	1680
Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly Leu Thr Gly Pro Arg	
545 550 555	
tgt gac cag tgc cag cga ggc tac tgc aat cgc tac ccg gtg tgc gtg	1728
Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg Tyr Pro Val Cys Val	
560 565 570	

gcc tgc cac cct tgc ttc cag acc tat gat gcg gac ctc cgg gag cag	1776
Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu Arg Glu Gln	
575 580 585 590	
gcc ctg cgc ttt ggt aga ctc cgg aat gcc acc gcc agc ctg tgg tca	1824
Ala Leu Arg Phe Gly Arg Leu Arg Asn Ala Thr Ala Ser Leu Trp Ser	
595 600 605	
ggg cct ggg ctg gag gac cgt ggc ctg gcc tcc cgg atc cta gat gca	1872
Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile Leu Asp Ala	
610 615 620	
aag agt aag att gag cag atc cga gca gtt ctc agc agc ccc gca gtc	1920
Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser Pro Ala Val	
625 630 635	
aca gag cag gag gtg gct cag gtg gcc agt gcc atc ctc tcc ctc agg	1968
Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu Ser Leu Arg	
640 645 650	
cga act ctc cag ggc ctg cag ctg gat ctg ccc ctg gag gag gag acg	2016
Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu Glu Thr	
655 660 665 670	
ttg tcc ctt ccg aga gac ctg gag agt ctt gac aga agc ttc aat ggt	2064
Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe Asn Gly	
675 680 685	
ctc ctt act atg tat cag agg aag agg gag cag ttt gaa aaa ata agc	2112
Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys Ile Ser	
690 695 700	
agt gct gat cct tca gga gcc ttc cgg atg ctg agc aca gcc tac gag	2160
Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu Ser Thr Ala Tyr Glu	
705 710 715	
cag tca gcc cag gct gct cag cag gtc tcc gac agc tcg cgc ctt ttg	2208
Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser Arg Leu Leu	
720 725 730	
gac cag ctc agg gac agc cgg aga gag gca gag agg ctg gtg cgg cag	2256
Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu Val Arg Gln	
735 740 745 750	
gcg gga gga gga gga ggc acc ggc agc ccc aag ctt gtg gcc ctg agg	2304
Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val Ala Leu Arg	
755 760 765	
ctg gag atg tct tcg ttg cct gac ctg aca ccc acc ttc aac aag ctc	2352
Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe Asn Lys Leu	
770 775 780	
tgt ggc aac tcc agg cag atg gct tgc acc cca ata tca tgc cct ggt	2400
Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser Cys Pro Gly	
785 790 795	
gag cta tgt ccc caa gac aat ggc aca gcc tgt ggc tcc cgc tgc agg	2448
Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys Gly Ser Arg Cys Arg	
800 805 810	
ggg gtc ctt ccc agg gcc ggt ggg gcc ttc ttg atg gcg ggg cag gtg	2496

Gly 815	Val	Leu	Pro	Arg	Ala 820	Gly	Gly	Ala	Phe	Leu 825	Met	Ala	Gly	Gln	Val 830	
gct	gag	cag	ctg	cgg	ggc	ttc	aat	gcc	cag	ctc	cag	cgg	acc	agg	cag	2544
Ala	Glu	Gln	Leu	Arg	Gly	Phe	Asn	Ala	Gln	Leu	Gln	Arg	Thr	Arg	Gln	
				835				840					845			
atg	att	agg	gca	gcc	gag	gaa	tct	gcc	tca	cag	att	caa	tcc	agt	gcc	2592
Met	Ile	Arg	Ala	Ala	Glu	Glu	Ser	Ala	Ser	Gln	Ile	Gln	Ser	Ser	Ala	
			850					855					860			
cag	cgc	ttg	gag	acc	cag	gtg	agc	gcc	agc	cgc	tcc	cag	atg	gag	gaa	2640
Gln	Arg	Leu	Glu	Thr	Gln	Val	Ser	Ala	Ser	Arg	Ser	Gln	Met	Glu	Glu	
		865					870					875				
gat	gtc	aga	cgc	aca	cgg	ctc	cta	atc	cag	cag	gtc	cgg	gac	ttc	cta	2688
Asp	Val	Arg	Arg	Thr	Arg	Leu	Leu	Ile	Gln	Gln	Val	Arg	Asp	Phe	Leu	
	880					885					890					
aca	gac	ccc	gac	act	gat	gca	gcc	act	atc	cag	gag	gtc	agc	gag	gcc	2736
Thr	Asp	Pro	Asp	Thr	Asp	Ala	Ala	Thr	Ile	Gln	Glu	Val	Ser	Glu	Ala	
895					900					905					910	
gtg	ctg	gcc	ctg	tgg	ctg	ccc	aca	gac	tca	gct	act	gtt	ctg	cag	aag	2784
Val	Leu	Ala	Leu	Trp	Leu	Pro	Thr	Asp	Ser	Ala	Thr	Val	Leu	Gln	Lys	
				915					920					925		
atg	aat	gag	atc	cag	gcc	att	gca	gcc	agg	ctc	ccc	aac	gtg	gac	ttg	2832
Met	Asn	Glu	Ile	Gln	Ala	Ile	Ala	Ala	Arg	Leu	Pro	Asn	Val	Asp	Leu	
			930					935					940			
gtg	ctg	tcc	cag	acc	aag	cag	gac	att	gcg	cgt	gcc	cgc	cgg	ttg	cag	2880
Val	Leu	Ser	Gln	Thr	Lys	Gln	Asp	Ile	Ala	Arg	Ala	Arg	Arg	Leu	Gln	
		945					950					955				
gct	gag	gct	gag	gaa	gcc	agg	agc	cga	gcc	cat	gca	gtg	gag	ggc	cag	2928
Ala	Glu	Ala	Glu	Glu	Ala	Arg	Ser	Arg	Ala	His	Ala	Val	Glu	Gly	Gln	
	960					965					970					
gtg	gaa	gat	gtg	gtt	ggg	aac	ctg	cgg	cag	ggg	aca	gtg	gca	ctg	cag	2976
Val	Glu	Asp	Val	Val	Gly	Asn	Leu	Arg	Gln	Gly	Thr	Val	Ala	Leu	Gln	
975					980					985					990	
gaa	gct	cag	gac	acc	atg	caa	ggc	acc	agc	cgc	tcc	ctt	cgg	ctt	atc	3024
Glu	Ala	Gln	Asp	Thr	Met	Gln	Gly	Thr	Ser	Arg	Ser	Leu	Arg	Leu	Ile	
				995					1000				1005			
cag	gac	agg	gtt	gct	gag	gtt	cag	cag	gta	ctg	cgg	cca	gca	gaa	aag	3072
Gln	Asp	Arg	Val	Ala	Glu	Val	Gln	Gln	Val	Leu	Arg	Pro	Ala	Glu	Lys	
			1010				1015					1020				
ctg	gtg	aca	agc	atg	acc	aag	cag	ctg	ggc	gac	ttc	tgg	aca	cgg	atg	3120
Leu	Val	Thr	Ser	Met	Thr	Lys	Gln	Leu	Gly	Asp	Phe	Trp	Thr	Arg	Met	
		1025					1030					1035				
gag	gag	ctc	cgc	cac	caa	gcc	cgg	cag	cag	ggg	gca	gag	gca	gtc	cag	3168
Glu	Glu	Leu	Arg	His	Gln	Ala	Arg	Gln	Gln	Gly	Ala	Glu	Ala	Val	Gln	
	1040					1045				1050						
gcc	cag	cag	ctt	gcg	gaa	ggc	gcc	agc	gag	cag	gca	ttg	agt	gcc	caa	3216
Ala	Gln	Gln	Leu	Ala	Glu	Gly	Ala	Ser	Glu	Gln	Ala	Leu	Ser	Ala	Gln	

1055	1060	1065	1070	
gag gga ttt gag aga ata aaa caa aag tat gct gag ttg aag gac cgg				3264
Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys Asp Arg				
	1075	1080	1085	
ttg ggt cag agt tcc atg ctg ggt gag cag ggt gcc cgg atc cag agt				3312
Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg Ile Gln Ser				
	1090	1095	1100	
gtg aag aca gag gca gag gag ctg ttt ggg gag acc atg gag atg atg				3360
Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu Thr Met Glu Met Met				
	1105	1110	1115	
gac agg atg aaa gac atg gag ttg gag ctg ctg cgg ggc agc cag gcc				3408
Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu Arg Gly Ser Gln Ala				
	1120	1125	1130	
atc atg ctg cgc tca gcg gac ctg aca gga ctg gag aag cgt gtg gag				3456
Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu Glu Lys Arg Val Glu				
	1135	1140	1145	1150
cag atc cgt gac cac atc aat ggg cgc gtg ctc tac tat gcc acc tgc				3504
Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu Tyr Tyr Ala Thr Cys				
	1155	1160	1165	
aag tgat				3511
Lys				
<210> 20				
<211> 1167				
<212> PRT				
<213> Homo sapiens				
<400> 20				
Leu Ala Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala Gln Gln Ala Cys				
1	5	10	15	
Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu Leu Val Gly Arg				
	20	25	30	
Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu Thr Lys Pro Glu				
	35	40	45	
Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys Cys Cys Lys Cys				
	50	55	60	
Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His Arg Val Glu Asn Val				
65	70	75	80	
Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln Ser Gln Asn Asp Val				
	85	90	95	
Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg Arg Phe Gln Leu Gln				
	100	105	110	
Glu Val Met Met Glu Phe Gln Gly Pro Met Pro Ala Gly Met Leu Ile				
	115	120	125	
Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg Val Tyr Gln Tyr Leu				

130	135	140
Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val Arg Gln Gly Arg Pro 145	150	155 160
Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu Pro Gln Arg Pro Asn 165	170	175
Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn Leu Met Asp Leu Val 180	185	190
Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile Gln Glu Val Gly Glu 195	200	205
Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu Ala Pro Val Pro Gln 210	215	220
Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala Val Ser Gln Leu Arg 225	230	235 240
Leu Gln Gly Ser Cys Phe Cys His Gly His Ala Asp Arg Cys Ala Pro 245	250	255
Lys Pro Gly Ala Ser Ala Gly Pro Ser Thr Ala Val Gln Val His Asp 260	265	270
Val Cys Val Cys Gln His Asn Thr Ala Gly Pro Asn Cys Glu Arg Cys 275	280	285
Ala Pro Phe Tyr Asn Asn Arg Pro Trp Arg Pro Ala Glu Gly Gln Asp 290	295	300
Ala His Glu Cys Gln Arg Cys Asp Cys Asn Gly His Ser Glu Thr Cys 305	310	315 320
His Phe Asp Pro Ala Val Phe Ala Ala Ser Gln Gly Ala Tyr Gly Gly 325	330	335
Val Cys Asp Asn Cys Arg Asp His Thr Glu Gly Lys Asn Cys Glu Arg 340	345	350
Cys Gln Leu His Tyr Phe Arg Asn Arg Arg Pro Gly Ala Ser Ile Gln 355	360	365
Glu Thr Cys Ile Ser Cys Glu Cys Asp Pro Asp Gly Ala Val Pro Gly 370	375	380
Ala Pro Cys Asp Pro Val Thr Gly Gln Cys Val Cys Lys Glu His Val 385	390	395 400
Gln Gly Glu Arg Cys Asp Leu Cys Lys Pro Gly Phe Thr Gly Leu Thr 405	410	415
Tyr Ala Asn Pro Gln Gly Cys His Arg Cys Asp Cys Asn Ile Leu Gly 420	425	430
Ser Arg Arg Asp Met Pro Cys Asp Glu Glu Ser Gly Arg Cys Leu Cys 435	440	445
Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln Cys Ala Pro Tyr His 450	455	460

Trp Lys Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys Ala Cys Asp Pro
465 470 475 480

His Asn Ser Leu Ser Pro Gln Cys Asn Gln Phe Thr Gly Gln Cys Pro
485 490 495

Cys Arg Glu Gly Phe Gly Gly Leu Met Cys Ser Ala Ala Ala Ile Arg
500 505 510

Gln Cys Pro Asp Arg Thr Tyr Gly Asp Val Ala Thr Gly Cys Arg Ala
515 520 525

Cys Asp Cys Asp Phe Arg Gly Thr Glu Gly Pro Gly Cys Asp Lys Ala
530 535 540

Ser Gly Arg Cys Leu Cys Arg Pro Gly Leu Thr Gly Pro Arg Cys Asp
545 550 555 560

Gln Cys Gln Arg Gly Tyr Cys Asn Arg Tyr Pro Val Cys Val Ala Cys
565 570 575

His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu Arg Glu Gln Ala Leu
580 585 590

Arg Phe Gly Arg Leu Arg Asn Ala Thr Ala Ser Leu Trp Ser Gly Pro
595 600 605

Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile Leu Asp Ala Lys Ser
610 615 620

Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser Pro Ala Val Thr Glu
625 630 635 640

Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu Ser Leu Arg Arg Thr
645 650 655

Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu Glu Thr Leu Ser
660 665 670

Leu Pro Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe Asn Gly Leu Leu
675 680 685

Thr Met Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys Ile Ser Ser Ala
690 695 700

Asp Pro Ser Gly Ala Phe Arg Met Leu Ser Thr Ala Tyr Glu Gln Ser
705 710 715 720

Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser Arg Leu Leu Asp Gln
725 730 735

Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu Val Arg Gln Ala Gly
740 745 750

Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val Ala Leu Arg Leu Glu
755 760 765

Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe Asn Lys Leu Cys Gly
770 775 780

Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser Cys Pro Gly Glu Leu
785 790 795 800

Cys Pro Gln Asp Asn Gly Thr Ala Cys Gly Ser Arg Cys Arg Gly Val
805 810 815

Leu Pro Arg Ala Gly Gly Ala Phe Leu Met Ala Gly Gln Val Ala Glu
820 825 830

Gln Leu Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr Arg Gln Met Ile
835 840 845

Arg Ala Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser Ser Ala Gln Arg
850 855 860

Leu Glu Thr Gln Val Ser Ala Ser Arg Ser Gln Met Glu Glu Asp Val
865 870 875 880

Arg Arg Thr Arg Leu Leu Ile Gln Gln Val Arg Asp Phe Leu Thr Asp
885 890 895

Pro Asp Thr Asp Ala Ala Thr Ile Gln Glu Val Ser Glu Ala Val Leu
900 905 910

Ala Leu Trp Leu Pro Thr Asp Ser Ala Thr Val Leu Gln Lys Met Asn
915 920 925

Glu Ile Gln Ala Ile Ala Ala Arg Leu Pro Asn Val Asp Leu Val Leu
930 935 940

Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg Leu Gln Ala Glu
945 950 955 960

Ala Glu Glu Ala Arg Ser Arg Ala His Ala Val Glu Gly Gln Val Glu
965 970 975

Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val Ala Leu Gln Glu Ala
980 985 990

Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu Arg Leu Ile Gln Asp
995 1000 1005

Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro Ala Glu Lys Leu Val
1010 1015 1020

Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp Thr Arg Met Glu Glu
1025 1030 1035 1040

Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu Ala Val Gln Ala Gln
1045 1050 1055

Gln Leu Ala Glu Gly Ala Ser Glu Gln Ala Leu Ser Ala Gln Glu Gly
1060 1065 1070

Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys Asp Arg Leu Gly
1075 1080 1085

Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg Ile Gln Ser Val Lys
1090 1095 1100

Thr Glu Ala Glu Glu Leu Phe Gly Glu Thr Met Glu Met Met Asp Arg

105		1110		1115		1120										
Met	Lys	Asp	Met	Glu	Leu	Glu	Leu	Leu	Arg	Gly	Ser	Gln	Ala	Ile	Met	
			1125					1130						1135		
Leu	Arg	Ser	Ala	Asp	Leu	Thr	Gly	Leu	Glu	Lys	Arg	Val	Glu	Gln	Ile	
		1140					1145					1150				
Arg	Asp	His	Ile	Asn	Gly	Arg	Val	Leu	Tyr	Tyr	Ala	Thr	Cys	Lys		
	1155				1160						1165					
<p><210> 21</p> <p><211> 3585</p> <p><212> DNA</p> <p><213> Homo sapiens</p> <p><220></p> <p><221> CDS</p> <p><222> (60)..(3581)</p> <p><220></p> <p><221> sig_peptide</p> <p><222> (60)..(116)</p> <p><400> 21</p>																
gttttaaactt aagcttctgc ctgccgcctg cctgcctgcc actgaggggtt cccagcacc															59	
atg	agg	gcc	tgg	atc	ttc	ttt	ctc	ctt	tgc	ctg	gcc	ggg	agg	gct	ctg	107
Met	Arg	Ala	Trp	Ile	Phe	Phe	Leu	Leu	Cys	Leu	Ala	Gly	Arg	Ala	Leu	
1				5					10					15		
gca	gcc	cca	caa	caa	gcc	tgc	tcc	cgt	ggg	gcc	tgc	tat	cca	cct	gtt	155
Ala	Ala	Pro	Gln	Gln	Ala	Cys	Ser	Arg	Gly	Ala	Cys	Tyr	Pro	Pro	Val	
			20					25					30			
ggg	gac	ctg	ctt	gtt	ggg	agg	acc	cgg	ttt	ctc	cga	gct	tca	tct	acc	203
Gly	Asp	Leu	Leu	Val	Gly	Arg	Thr	Arg	Phe	Leu	Arg	Ala	Ser	Ser	Thr	
		35				40						45				
tgt	gga	ctg	acc	aag	cct	gag	acc	tac	tgc	acc	cag	tat	ggc	gag	tgg	251
Cys	Gly	Leu	Thr	Lys	Pro	Glu	Thr	Tyr	Cys	Thr	Gln	Tyr	Gly	Glu	Trp	
	50					55					60					
cag	atg	aaa	tgc	tgc	aag	tgt	gac	tcc	agg	cag	cct	cac	aac	tac	tac	299
Gln	Met	Lys	Cys	Cys	Lys	Cys	Asp	Ser	Arg	Gln	Pro	His	Asn	Tyr	Tyr	
65					70					75				80		
agt	cac	cga	gta	gag	aat	gtg	gct	tca	tcc	tcc	ggc	ccc	atg	cgc	tgg	347
Ser	His	Arg	Val	Glu	Asn	Val	Ala	Ser	Ser	Ser	Gly	Pro	Met	Arg	Trp	
			85					90					95			
tgg	cag	tcc	cag	aat	gat	gtg	aac	cct	gtc	tct	ctg	cag	ctg	gac	ctg	395
Trp	Gln	Ser	Gln	Asn	Asp	Val	Asn	Pro	Val	Ser	Leu	Gln	Leu	Asp	Leu	
			100					105					110			
gac	agg	aga	ttc	cag	ctt	caa	gaa	gtc	atg	atg	gag	ttc	cag	ggg	ccc	443
Asp	Arg	Arg	Phe	Gln	Leu	Gln	Glu	Val	Met	Met	Glu	Phe	Gln	Gly	Pro	
		115					120					125				
atg	cct	gcc	ggc	atg	ctg	att	gag	cgc	tcc	tca	gac	ttc	ggt	aag	acc	491

Met	Pro	Ala	Gly	Met	Leu	Ile	Glu	Arg	Ser	Ser	Asp	Phe	Gly	Lys	Thr	
130						135					140					
tgg	cga	gtg	tac	cag	tac	ctg	gct	gcc	gac	tgc	acc	tcc	acc	ttc	cct	539
Trp	Arg	Val	Tyr	Gln	Tyr	Leu	Ala	Ala	Asp	Cys	Thr	Ser	Thr	Phe	Pro	
145					150					155					160	
cgg	gtc	cgc	cag	ggc	cgg	cct	cag	agc	tgg	cag	gat	gtt	cgg	tgc	cag	587
Arg	Val	Arg	Gln	Gly	Arg	Pro	Gln	Ser	Trp	Gln	Asp	Val	Arg	Cys	Gln	
				165					170					175		
tcc	ctg	cct	cag	agg	cct	aat	gca	cgc	cta	aat	ggg	ggg	aag	gtc	caa	635
Ser	Leu	Pro	Gln	Arg	Pro	Asn	Ala	Arg	Leu	Asn	Gly	Gly	Lys	Val	Gln	
			180				185						190			
ctt	aac	ctt	atg	gat	tta	gtg	tct	ggg	att	cca	gca	act	caa	agt	caa	683
Leu	Asn	Leu	Met	Asp	Leu	Val	Ser	Gly	Ile	Pro	Ala	Thr	Gln	Ser	Gln	
		195				200						205				
aaa	att	caa	gag	gtg	ggg	gag	atc	aca	aac	ttg	aga	gtc	aat	ttc	acc	731
Lys	Ile	Gln	Glu	Val	Gly	Glu	Ile	Thr	Asn	Leu	Arg	Val	Asn	Phe	Thr	
	210					215					220					
agg	ctg	gcc	cct	gtg	ccc	caa	agg	ggc	tac	cac	cct	ccc	agc	gcc	tac	779
Arg	Leu	Ala	Pro	Val	Pro	Gln	Arg	Gly	Tyr	His	Pro	Pro	Ser	Ala	Tyr	
225					230				235						240	
tat	gct	gtg	tcc	cag	ctc	cgt	ctg	cag	ggg	agc	tgc	ttc	tgt	cac	ggc	827
Tyr	Ala	Val	Ser	Gln	Leu	Arg	Leu	Gln	Gly	Ser	Cys	Phe	Cys	His	Gly	
				245					250					255		
cat	gct	gat	cgc	tgc	gca	ccc	aag	cct	ggg	gcc	tct	gca	ggc	ccc	tcc	875
His	Ala	Asp	Arg	Cys	Ala	Pro	Lys	Pro	Gly	Ala	Ser	Ala	Gly	Pro	Ser	
			260				265						270			
acc	gct	gtg	cag	gtc	cac	gat	gtc	tgc	gtc	tgc	cag	cac	aac	act	gcc	923
Thr	Ala	Val	Gln	Val	His	Asp	Val	Cys	Val	Cys	Gln	His	Asn	Thr	Ala	
		275					280					285				
ggc	cca	aat	tgt	gag	cgc	tgt	gca	ccc	ttc	tac	aac	aac	cgg	ccc	tgg	971
Gly	Pro	Asn	Cys	Glu	Arg	Cys	Ala	Pro	Phe	Tyr	Asn	Asn	Arg	Pro	Trp	
	290					295					300					
aga	ccg	gcg	gag	ggc	cag	gac	gcc	cat	gaa	tgc	caa	agg	tgc	gac	tgc	1019
Arg	Pro	Ala	Glu	Gly	Gln	Asp	Ala	His	Glu	Cys	Gln	Arg	Cys	Asp	Cys	
305					310					315					320	
aat	ggg	cac	tca	gag	aca	tgt	cac	ttt	gac	ccc	gct	gtg	ttt	gcc	gcc	1067
Asn	Gly	His	Ser	Glu	Thr	Cys	His	Phe	Asp	Pro	Ala	Val	Phe	Ala	Ala	
				325					330					335		
agc	cag	ggg	gca	tat	gga	ggc	gtg	tgt	gac	aat	tgc	cgg	gac	cac	acc	1115
Ser	Gln	Gly	Ala	Tyr	Gly	Gly	Val	Cys	Asp	Asn	Cys	Arg	Asp	His	Thr	
			340				345						350			
gaa	ggc	aag	aac	tgt	gag	cgg	tgt	cag	ctg	cac	tat	ttc	cgg	aac	cgg	1163
Glu	Gly	Lys	Asn	Cys	Glu	Arg	Cys	Gln	Leu	His	Tyr	Phe	Arg	Asn	Arg	
		355					360					365				
cgc	ccg	gga	gct	tcc	att	cag	gag	acc	tgc	atc	tcc	tgc	gag	tgt	gat	1211
Arg	Pro	Gly	Ala	Ser	Ile	Gln	Glu	Thr	Cys	Ile	Ser	Cys	Glu	Cys	Asp	

370	375	380	
ccg gat ggg gca gtg cca ggg gct ccc tgt gac cca gtg acc ggg cag			1259
Pro Asp Gly Ala Val Pro Gly Ala Pro Cys Asp Pro Val Thr Gly Gln			
385	390	395	400
tgt gtg tgc aag gag cat gtg cag gga gag cgc tgt gac cta tgc aag			1307
Cys Val Cys Lys Glu His Val Gln Gly Glu Arg Cys Asp Leu Cys Lys			
	405	410	415
ccg ggc ttc act gga ctc acc tac gcc aac ccg cag ggc tgc cac cgc			1355
Pro Gly Phe Thr Gly Leu Thr Tyr Ala Asn Pro Gln Gly Cys His Arg			
	420	425	430
tgt gac tgc aac atc ctg ggg tcc cgg agg gac atg ccg tgt gac gag			1403
Cys Asp Cys Asn Ile Leu Gly Ser Arg Arg Asp Met Pro Cys Asp Glu			
	435	440	445
gag agt ggg cgc tgc ctt tgt ctg ccc aac gtg gtg ggt ccc aaa tgt			1451
Glu Ser Gly Arg Cys Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys			
	450	455	460
gac cag tgt gct ccc tac cac tgg aag ctg gcc agt ggc cag ggc tgt			1499
Asp Gln Cys Ala Pro Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys			
465	470	475	480
gaa ccg tgt gcc tgc gac ccg cac aac tcc ctc agc cca cag tgc aac			1547
Glu Pro Cys Ala Cys Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn			
	485	490	495
cag ttc aca ggg cag tgc ccc tgt cgg gaa ggc ttt ggt ggc ctg atg			1595
Gln Phe Thr Gly Gln Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met			
	500	505	510
tgc agc gct gca gcc atc cgc cag tgt cca gac cgg acc tat gga gac			1643
Cys Ser Ala Ala Ala Ile Arg Gln Cys Pro Asp Arg Thr Tyr Gly Asp			
	515	520	525
gtg gcc aca gga tgc cga gcc tgt gac tgt gat ttc cgg gga aca gag			1691
Val Ala Thr Gly Cys Arg Ala Cys Asp Cys Asp Phe Arg Gly Thr Glu			
	530	535	540
ggc ccg ggc tgc gac aag gca tca ggc cgc tgc ctc tgc cgc cct ggc			1739
Gly Pro Gly Cys Asp Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly			
545	550	555	560
ttg acc ggg ccc cgc tgt gac cag tgc cag cga ggc tac tgc aat cgc			1787
Leu Thr Gly Pro Arg Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg			
	565	570	575
tac ccg gtg tgc gtg gcc tgc cac cct tgc ttc cag acc tat gat gcg			1835
Tyr Pro Val Cys Val Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala			
	580	585	590
gac ctc cgg gag cag gcc ctg cgc ttt ggt aga ctc cgg aat gcc acc			1883
Asp Leu Arg Glu Gln Ala Leu Arg Phe Gly Arg Leu Arg Asn Ala Thr			
	595	600	605
gcc agc ctg tgg tca ggg cct ggg ctg gag gac cgt ggc ctg gcc tcc			1931
Ala Ser Leu Trp Ser Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser			
	610	615	620

cgg atc cta gat gca aag agt aag att gag cag atc cga gca gtt ctc	1979
Arg Ile Leu Asp Ala Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu	
625 630 635 640	
agc agc ccc gca gtc aca gag cag gag gtg gct cag gtg gcc agt gcc	2027
Ser Ser Pro Ala Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala	
645 650 655	
atc ctc tcc ctc agg cga act ctc cag ggc ctg cag ctg gat ctg ccc	2075
Ile Leu Ser Leu Arg Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro	
660 665 670	
ctg gag gag gag acg ttg tcc ctt ccg aga gac ctg gag agt ctt gac	2123
Leu Glu Glu Glu Thr Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp	
675 680 685	
aga agc ttc aat ggt ctc ctt act atg tat cag agg aag agg gag cag	2171
Arg Ser Phe Asn Gly Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln	
690 695 700	
ttt gaa aaa ata agc agt gct gat cct tca gga gcc ttc cgg atg ctg	2219
Phe Glu Lys Ile Ser Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu	
705 710 715 720	
agc aca gcc tac gag cag tca gcc cag gct gct cag cag gtc tcc gac	2267
Ser Thr Ala Tyr Glu Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp	
725 730 735	
agc tcg cgc ctt ttg gac cag ctc agg gac agc cgg aga gag gca gag	2315
Ser Ser Arg Leu Leu Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu	
740 745 750	
agg ctg gtg cgg cag gcg gga gga gga gga ggc acc ggc agc ccc aag	2363
Arg Leu Val Arg Gln Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys	
755 760 765	
ctt gtg gcc ctg agg ctg gag atg tct tcg ttg cct gac ctg aca ccc	2411
Leu Val Ala Leu Arg Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro	
770 775 780	
acc ttc aac aag ctc tgt ggc aac tcc agg cag atg gct tgc acc cca	2459
Thr Phe Asn Lys Leu Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro	
785 790 795 800	
ata tca tgc cct ggt gag cta tgt ccc caa gac aat ggc aca gcc tgt	2507
Ile Ser Cys Pro Gly Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys	
805 810 815	
ggc tcc cgc tgc agg ggt gtc ctt ccc agg gcc ggt ggg gcc ttc ttg	2555
Gly Ser Arg Cys Arg Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu	
820 825 830	
atg gcg ggg cag gtg gct gag cag ctg cgg ggc ttc aat gcc cag ctc	2603
Met Ala Gly Gln Val Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu	
835 840 845	
cag cgg acc agg cag atg att agg gca gcc gag gaa tct gcc tca cag	2651
Gln Arg Thr Arg Gln Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln	
850 855 860	

att caa tcc agt gcc cag cgc ttg gag acc cag gtg agc gcc agc cgc	2699
Ile Gln Ser Ser Ala Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg	
865 870 875 880	
tcc cag atg gag gaa gat gtc aga cgc aca cgg ctc cta atc cag cag	2747
Ser Gln Met Glu Glu Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln	
885 890 895	
gtc cgg gac ttc cta aca gac ccc gac act gat gca gcc act atc cag	2795
Val Arg Asp Phe Leu Thr Asp Pro Asp Thr Asp Ala Ala Thr Ile Gln	
900 905 910	
gag gtc agc gag gcc gtg ctg gcc ctg tgg ctg ccc aca gac tca gct	2843
Glu Val Ser Glu Ala Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala	
915 920 925	
act gtt ctg cag aag atg aat gag atc cag gcc att gca gcc agg ctc	2891
Thr Val Leu Gln Lys Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu	
930 935 940	
ccc aac gtg gac ttg gtg ctg tcc cag acc aag cag gac att gcg cgt	2939
Pro Asn Val Asp Leu Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg	
945 950 955 960	
gcc cgc cgg ttg cag gct gag gct gag gaa gcc agg agc cga gcc cat	2987
Ala Arg Arg Leu Gln Ala Glu Ala Glu Ala Arg Ser Arg Ala His	
965 970 975	
gca gtg gag ggc cag gtg gaa gat gtg gtt ggg aac ctg cgg cag ggg	3035
Ala Val Glu Gly Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly	
980 985 990	
aca gtg gca ctg cag gaa gct cag gac acc atg caa ggc acc agc cgc	3083
Thr Val Ala Leu Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg	
995 1000 1005	
tcc ctt cgg ctt atc cag gac agg gtt gct gag gtt cag cag gta ctg	3131
Ser Leu Arg Leu Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu	
1010 1015 1020	
cgg cca gca gaa aag ctg gtg aca agc atg acc aag cag ctg ggt gac	3179
Arg Pro Ala Glu Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp	
1025 1030 1035 1040	
ttc tgg aca cgg atg gag gag ctc cgc cac caa gcc cgg cag cag ggg	3227
Phe Trp Thr Arg Met Glu Glu Leu Arg His Gln Ala Arg Gln Gln Gly	
1045 1050 1055	
gca gag gca gtc cag gcc cag cag ctt gcg gaa ggt gcc agc gag cag	3275
Ala Glu Ala Val Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln	
1060 1065 1070	
gca ttg agt gcc caa gag gga ttt gag aga ata aaa caa aag tat gct	3323
Ala Leu Ser Ala Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala	
1075 1080 1085	
gag ttg aag gac cgg ttg ggt cag agt tcc atg ctg ggt gag cag ggt	3371
Glu Leu Lys Asp Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly	
1090 1095 1100	
gcc cgg atc cag agt gtg aag aca gag gca gag gag ctg ttt ggg gag	3419

Ala Arg Ile Gln Ser Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu
 1105 1110 1115 1120

acc atg gag atg atg gac agg atg aaa gac atg gag ttg gag ctg ctg 3467
 Thr Met Glu Met Met Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu
 1125 1130 1135

cgg ggc agc cag gcc atc atg ctg cgc tca gcg gac ctg aca gga ctg 3515
 Arg Gly Ser Gln Ala Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu
 1140 1145 1150

gag aag cgt gtg gag cag atc cgt gac cac atc aat ggg cgc gtg ctc 3563
 Glu Lys Arg Val Glu Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu
 1155 1160 1165

tac tat gcc acc tgc aag tgat 3585
 Tyr Tyr Ala Thr Cys Lys
 1170

<210> 22
 <211> 1174
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 1 5 10 15

Ala Ala Pro Gln Gln Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val
 20 25 30

Gly Asp Leu Leu Val Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr
 35 40 45

Cys Gly Leu Thr Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp
 50 55 60

Gln Met Lys Cys Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr
 65 70 75 80

Ser His Arg Val Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp
 85 90 95

Trp Gln Ser Gln Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu
 100 105 110

Asp Arg Arg Phe Gln Leu Gln Glu Val Met Met Glu Phe Gln Gly Pro
 115 120 125

Met Pro Ala Gly Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr
 130 135 140

Trp Arg Val Tyr Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro
 145 150 155 160

Arg Val Arg Gln Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln
 165 170 175

Ser Leu Pro Gln Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln
 180 185 190

Leu Asn Leu Met Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln
195 200 205

Lys Ile Gln Glu Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr
210 215 220

Arg Leu Ala Pro Val Pro Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr
225 230 235 240

Tyr Ala Val Ser Gln Leu Arg Leu Gln Gly Ser Cys Phe Cys His Gly
245 250 255

His Ala Asp Arg Cys Ala Pro Lys Pro Gly Ala Ser Ala Gly Pro Ser
260 265 270

Thr Ala Val Gln Val His Asp Val Cys Val Cys Gln His Asn Thr Ala
275 280 285

Gly Pro Asn Cys Glu Arg Cys Ala Pro Phe Tyr Asn Asn Arg Pro Trp
290 295 300

Arg Pro Ala Glu Gly Gln Asp Ala His Glu Cys Gln Arg Cys Asp Cys
305 310 315 320

Asn Gly His Ser Glu Thr Cys His Phe Asp Pro Ala Val Phe Ala Ala
325 330 335

Ser Gln Gly Ala Tyr Gly Gly Val Cys Asp Asn Cys Arg Asp His Thr
340 345 350

Glu Gly Lys Asn Cys Glu Arg Cys Gln Leu His Tyr Phe Arg Asn Arg
355 360 365

Arg Pro Gly Ala Ser Ile Gln Glu Thr Cys Ile Ser Cys Glu Cys Asp
370 375 380

Pro Asp Gly Ala Val Pro Gly Ala Pro Cys Asp Pro Val Thr Gly Gln
385 390 395 400

Cys Val Cys Lys Glu His Val Gln Gly Glu Arg Cys Asp Leu Cys Lys
405 410 415

Pro Gly Phe Thr Gly Leu Thr Tyr Ala Asn Pro Gln Gly Cys His Arg
420 425 430

Cys Asp Cys Asn Ile Leu Gly Ser Arg Arg Asp Met Pro Cys Asp Glu
435 440 445

Glu Ser Gly Arg Cys Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys
450 455 460

Asp Gln Cys Ala Pro Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys
465 470 475 480

Glu Pro Cys Ala Cys Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn
485 490 495

Gln Phe Thr Gly Gln Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met
500 505 510

Cys Ser Ala Ala Ala Ile Arg Gln Cys Pro Asp Arg Thr Tyr Gly Asp
515 520 525

Val Ala Thr Gly Cys Arg Ala Cys Asp Cys Asp Phe Arg Gly Thr Glu
530 535 540

Gly Pro Gly Cys Asp Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly
545 550 555 560

Leu Thr Gly Pro Arg Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg
565 570 575

Tyr Pro Val Cys Val Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala
580 585 590

Asp Leu Arg Glu Gln Ala Leu Arg Phe Gly Arg Leu Arg Asn Ala Thr
595 600 605

Ala Ser Leu Trp Ser Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser
610 615 620

Arg Ile Leu Asp Ala Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu
625 630 635 640

Ser Ser Pro Ala Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala
645 650 655

Ile Leu Ser Leu Arg Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro
660 665 670

Leu Glu Glu Glu Thr Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp
675 680 685

Arg Ser Phe Asn Gly Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln
690 695 700

Phe Glu Lys Ile Ser Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu
705 710 715 720

Ser Thr Ala Tyr Glu Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp
725 730 735

Ser Ser Arg Leu Leu Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu
740 745 750

Arg Leu Val Arg Gln Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys
755 760 765

Leu Val Ala Leu Arg Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro
770 775 780

Thr Phe Asn Lys Leu Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro
785 790 795 800

Ile Ser Cys Pro Gly Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys
805 810 815

Gly Ser Arg Cys Arg Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu
820 825 830

Met Ala Gly Gln Val Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu

835 840 845

Gln Arg Thr Arg Gln Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln
850 855 860

Ile Gln Ser Ser Ala Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg
865 870 875 880

Ser Gln Met Glu Glu Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln
885 890 895

Val Arg Asp Phe Leu Thr Asp Pro Asp Thr Asp Ala Ala Thr Ile Gln
900 905 910

Glu Val Ser Glu Ala Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala
915 920 925

Thr Val Leu Gln Lys Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu
930 935 940

Pro Asn Val Asp Leu Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg
945 950 955 960

Ala Arg Arg Leu Gln Ala Glu Ala Glu Glu Ala Arg Ser Arg Ala His
965 970 975

Ala Val Glu Gly Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly
980 985 990

Thr Val Ala Leu Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg
995 1000 1005

Ser Leu Arg Leu Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu
1010 1015 1020

Arg Pro Ala Glu Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp
1025 1030 1035 1040

Phe Trp Thr Arg Met Glu Glu Leu Arg His Gln Ala Arg Gln Gln Gly
1045 1050 1055

Ala Glu Ala Val Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln
1060 1065 1070

Ala Leu Ser Ala Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala
1075 1080 1085

Glu Leu Lys Asp Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly
1090 1095 1100

Ala Arg Ile Gln Ser Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu
1105 1110 1115 1120

Thr Met Glu Met Met Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu
1125 1130 1135

Arg Gly Ser Gln Ala Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu
1140 1145 1150

Glu Lys Arg Val Glu Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu
1155 1160 1165

Tyr Tyr Ala Thr Cys Lys
1170

<210> 23
<211> 3469
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (3465)

<400> 23
caa caa gcc tgc tcc cgt ggg gcc tgc tat cca cct gtt ggg gac ctg 48
Gln Gln Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu
1 5 10 15
ctt gtt ggg agg acc cgg ttt ctc cga gct tca tct acc tgt gga ctg 96
Leu Val Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu
20 25 30
acc aag cct gag acc tac tgc acc cag tat ggc gag tgg cag atg aaa 144
Thr Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys
35 40 45
tgc tgc aag tgt gac tcc agg cag cct cac aac tac tac agt cac cga 192
Cys Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His Arg
50 55 60
gta gag aat gtg gct tca tcc tcc ggc ccc atg cgc tgg tgg cag tcc 240
Val Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln Ser
65 70 75 80
cag aat gat gtg aac cct gtc tct ctg cag ctg gac ctg gac agg aga 288
Gln Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg Arg
85 90 95
ttc cag ctt caa gaa gtc atg atg gag ttc cag ggg ccc atg cct gcc 336
Phe Gln Leu Gln Glu Val Met Met Glu Phe Gln Gly Pro Met Pro Ala
100 105 110
ggc atg ctg att gag cgc tcc tca gac ttc ggt aag acc tgg cga gtg 384
Gly Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg Val
115 120 125
tac cag tac ctg gct gcc gac tgc acc tcc acc ttc cct cgg gtc cgc 432
Tyr Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val Arg
130 135 140
cag ggt cgg cct cag agc tgg cag gat gtt cgg tgc cag tcc ctg cct 480
Gln Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu Pro
145 150 155 160
cag agg cct aat gca cgc cta aat ggg ggg aag gtc caa ctt aac ctt 528
Gln Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn Leu
165 170 175
atg gat tta gtg tct ggg att cca gca act caa agt caa aaa att caa 576
Met Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile Gln

180							185					190					
gag	gtg	ggg	gag	atc	aca	aac	ttg	aga	gtc	aat	ttc	acc	agg	ctg	gcc	624	
Glu	Val	Gly	Glu	Ile	Thr	Asn	Leu	Arg	Val	Asn	Phe	Thr	Arg	Leu	Ala		
		195					200					205					
cct	gtg	ccc	caa	agg	ggc	tac	cac	cct	ccc	agc	gcc	tac	tat	gct	gtg	672	
Pro	Val	Pro	Gln	Arg	Gly	Tyr	His	Pro	Pro	Ser	Ala	Tyr	Tyr	Ala	Val		
	210					215					220						
tcc	cag	ctc	cgt	ctg	cag	ggg	agc	tgc	ttc	tgt	cac	ggc	cat	gct	gat	720	
Ser	Gln	Leu	Arg	Leu	Gln	Gly	Ser	Cys	Phe	Cys	His	Gly	His	Ala	Asp		
225					230					235					240		
cgc	tgc	gca	ccc	aag	cct	ggg	gcc	tct	gca	ggc	ccc	tcc	acc	gct	gtg	768	
Arg	Cys	Ala	Pro	Lys	Pro	Gly	Ala	Ser	Ala	Gly	Pro	Ser	Thr	Ala	Val		
				245					250					255			
cag	gtc	cac	gat	gtc	tgc	gtc	tgc	cag	cac	aac	act	gcc	ggc	cca	aat	816	
Gln	Val	His	Asp	Val	Cys	Val	Cys	Gln	His	Asn	Thr	Ala	Gly	Pro	Asn		
			260					265					270				
tgt	gag	cgc	tgt	gca	ccc	ttc	tac	aac	aac	cgg	ccc	tgg	aga	ccg	gcg	864	
Cys	Glu	Arg	Cys	Ala	Pro	Phe	Tyr	Asn	Asn	Arg	Pro	Trp	Arg	Pro	Ala		
		275					280					285					
gag	ggc	cag	gac	gcc	cat	gaa	tgc	caa	agg	tgc	gac	tgc	aat	ggg	cac	912	
Glu	Gly	Gln	Asp	Ala	His	Glu	Cys	Gln	Arg	Cys	Asp	Cys	Asn	Gly	His		
	290					295					300						
tca	gag	aca	tgt	cac	ttt	gac	ccc	gct	gtg	ttt	gcc	gcc	agc	cag	ggg	960	
Ser	Glu	Thr	Cys	His	Phe	Asp	Pro	Ala	Val	Phe	Ala	Ala	Ser	Gln	Gly		
305					310					315					320		
gca	tat	gga	ggt	gtg	tgt	gac	aat	tgc	cgg	gac	cac	acc	gaa	ggc	aag	1008	
Ala	Tyr	Gly	Gly	Val	Cys	Asp	Asn	Cys	Arg	Asp	His	Thr	Glu	Gly	Lys		
				325				330						335			
aac	tgt	gag	cgg	tgt	cag	ctg	cac	tat	ttc	cgg	aac	cgg	cgc	ccg	gga	1056	
Asn	Cys	Glu	Arg	Cys	Gln	Leu	His	Tyr	Phe	Arg	Asn	Arg	Arg	Pro	Gly		
			340					345					350				
gct	tcc	att	cag	gag	acc	tgc	atc	tcc	tgc	gag	tgt	gat	ccg	gat	ggg	1104	
Ala	Ser	Ile	Gln	Glu	Thr	Cys	Ile	Ser	Cys	Glu	Cys	Asp	Pro	Asp	Gly		
		355				360						365					
gca	gtg	cca	ggg	gct	ccc	tgt	gac	cca	gtg	acc	ggg	cag	tgt	gtg	tgc	1152	
Ala	Val	Pro	Gly	Ala	Pro	Cys	Asp	Pro	Val	Thr	Gly	Gln	Cys	Val	Cys		
	370					375					380						
aag	gag	cat	gtg	cag	gga	gag	cgc	tgt	gac	cta	tgc	aag	ccg	ggc	ttc	1200	
Lys	Glu	His	Val	Gln	Gly	Glu	Arg	Cys	Asp	Leu	Cys	Lys	Pro	Gly	Phe		
385					390					395					400		
act	gga	ctc	acc	tac	gcc	aac	ccg	cag	ggc	tgc	cac	cgc	tgt	gac	tgc	1248	
Thr	Gly	Leu	Thr	Tyr	Ala	Asn	Pro	Gln	Gly	Cys	His	Arg	Cys	Asp	Cys		
				405					410					415			
aac	atc	ctg	ggg	tcc	cgg	agg	gac	atg	ccg	tgt	gac	gag	gag	agt	ggg	1296	
Asn	Ile	Leu	Gly	Ser	Arg	Arg	Asp	Met	Pro	Cys	Asp	Glu	Glu	Ser	Gly		
			420					425						430			

cgc tgc ctt tgt ctg ccc aac gtg gtg ggt ccc aaa tgt gac cag tgt	1344
Arg Cys Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln Cys	
435 440 445	
gct ccc tac cac tgg aag ctg gcc agt ggc cag ggc tgt gaa ccg tgt	1392
Ala Pro Tyr His Trp Lys Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys	
450 455 460	
gcc tgc gac ccg cac aac tcc ctc agc cca cag tgc aac cag ttc aca	1440
Ala Cys Asp Pro His Asn Ser Leu Ser Pro Gln Cys Asn Gln Phe Thr	
465 470 475 480	
ggg cag tgc ccc tgt cgg gaa ggc ttt ggt ggc ctg atg tgc agc gct	1488
Gly Gln Cys Pro Cys Arg Glu Gly Phe Gly Gly Leu Met Cys Ser Ala	
485 490 495	
gca gcc atc cgc cag tgt cca gac cgg acc tat gga gac gtg gcc aca	1536
Ala Ala Ile Arg Gln Cys Pro Asp Arg Thr Tyr Gly Asp Val Ala Thr	
500 505 510	
gga tgc cga gcc tgt gac tgt gat ttc cgg gga aca gag ggc ccg ggc	1584
Gly Cys Arg Ala Cys Asp Cys Asp Phe Arg Gly Thr Glu Gly Pro Gly	
515 520 525	
tgc gac aag gca tca ggc cgc tgc ctc tgc cgc cct ggc ttg acc ggg	1632
Cys Asp Lys Ala Ser Gly Arg Cys Leu Cys Arg Pro Gly Leu Thr Gly	
530 535 540	
ccc cgc tgt gac cag tgc cag cga ggc tac tgc aat cgc tac ccg gtg	1680
Pro Arg Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Arg Tyr Pro Val	
545 550 555 560	
tgc gtg gcc tgc cac cct tgc ttc cag acc tat gat gcg gac ctc cgg	1728
Cys Val Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu Arg	
565 570 575	
gag cag gcc ctg cgc ttt ggt aga ctc cgg aat gcc acc gcc agc ctg	1776
Glu Gln Ala Leu Arg Phe Gly Arg Leu Arg Asn Ala Thr Ala Ser Leu	
580 585 590	
tgg tca ggg cct ggg ctg gag gac cgt ggc ctg gcc tcc cgg atc cta	1824
Trp Ser Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile Leu	
595 600 605	
gat gca aag agt aag att gag cag atc cga gca gtt ctc agc agc ccc	1872
Asp Ala Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser Pro	
610 615 620	
gca gtc aca gag cag gag gtg gct cag gtg gcc agt gcc atc ctc tcc	1920
Ala Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu Ser	
625 630 635 640	
ctc agg cga act ctc cag ggc ctg cag ctg gat ctg ccc ctg gag gag	1968
Leu Arg Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu	
645 650 655	
gag acg ttg tcc ctt ccg aga gac ctg gag agt ctt gac aga agc ttc	2016
Glu Thr Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe	
660 665 670	

aat ggt ctc ctt act atg tat cag agg aag agg gag cag ttt gaa aaa	2064
Asn Gly Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys	
675 680 685	
ata agc agt gct gat cct tca gga gcc ttc cgg atg ctg agc aca gcc	2112
Ile Ser Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu Ser Thr Ala	
690 695 700	
tac gag cag tca gcc cag gct gct cag cag gtc tcc gac agc tcg cgc	2160
Tyr Glu Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser Arg	
705 710 715 720	
ctt ttg gac cag ctc agg gac agc cgg aga gag gca gag agg ctg gtg	2208
Leu Leu Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu Val	
725 730 735	
cgg cag gcg gga gga gga gga ggc acc ggc agc ccc aag ctt gtg gcc	2256
Arg Gln Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val Ala	
740 745 750	
ctg agg ctg gag atg tct tcg ttg cct gac ctg aca ccc acc ttc aac	2304
Leu Arg Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe Asn	
755 760 765	
aag ctc tgt ggc aac tcc agg cag atg gct tgc acc cca ata tca tgc	2352
Lys Leu Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser Cys	
770 775 780	
cct ggt gag cta tgt ccc caa gac aat ggc aca gcc tgt ggc tcc cgc	2400
Pro Gly Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys Gly Ser Arg	
785 790 795 800	
tgc agg ggt gtc ctt ccc agg gcc ggt ggg gcc ttc ttg atg gcg ggg	2448
Cys Arg Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu Met Ala Gly	
805 810 815	
cag gtg gct gag cag ctg cgg ggc ttc aat gcc cag ctc cag cgg acc	2496
Gln Val Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr	
820 825 830	
agg cag atg att agg gca gcc gag gaa tct gcc tca cag att caa tcc	2544
Arg Gln Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser	
835 840 845	
agt gcc cag cgc ttg gag acc cag gtg agc gcc agc cgc tcc cag atg	2592
Ser Ala Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg Ser Gln Met	
850 855 860	
gag gaa gat gtc aga cgc aca cgg ctc cta atc cag cag gtc cgg gac	2640
Glu Glu Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln Val Arg Asp	
865 870 875 880	
ttc cta aca gac ccc gac act gat gca gcc act atc cag gag gtc agc	2688
Phe Leu Thr Asp Pro Asp Thr Asp Ala Ala Thr Ile Gln Glu Val Ser	
885 890 895	
gag gcc gtg ctg gcc ctg tgg ctg ccc aca gac tca gct act gtt ctg	2736
Glu Ala Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala Thr Val Leu	
900 905 910	
cag aag atg aat gag atc cag gcc att gca gcc agg ctc ccc aac gtg	2784

Gln Lys Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu Pro Asn Val	
915 920 925	
gac ttg gtg ctg tcc cag acc aag cag gac att gcg cgt gcc cgc cgg	2832
Asp Leu Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg	
930 935 940	
ttg cag gct gag gct gag gaa gcc agg agc cga gcc cat gca gtg gag	2880
Leu Gln Ala Glu Ala Glu Glu Ala Arg Ser Arg Ala His Ala Val Glu	
945 950 955 960	
ggc cag gtg gaa gat gtg gtt ggg aac ctg cgg cag ggg aca gtg gca	2928
Gly Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val Ala	
965 970 975	
ctg cag gaa gct cag gac acc atg caa ggc acc agc cgc tcc ctt cgg	2976
Leu Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu Arg	
980 985 990	
ctt atc cag gac agg gtt gct gag gtt cag cag gta ctg cgg cca gca	3024
Leu Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro Ala	
995 1000 1005	
gaa aag ctg gtg aca agc atg acc aag cag ctg ggt gac ttc tgg aca	3072
Glu Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp Thr	
1010 1015 1020	
cgg atg gag gag ctc cgc cac caa gcc cgg cag cag ggg gca gag gca	3120
Arg Met Glu Glu Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu Ala	
1025 1030 1035 1040	
gtc cag gcc cag cag ctt gcg gaa ggt gcc agc gag cag gca ttg agt	3168
Val Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln Ala Leu Ser	
1045 1050 1055	
gcc caa gag gga ttt gag aga ata aaa caa aag tat gct gag ttg aag	3216
Ala Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys	
1060 1065 1070	
gac cgg ttg ggt cag agt tcc atg ctg ggt gag cag ggt gcc cgg atc	3264
Asp Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg Ile	
1075 1080 1085	
cag agt gtg aag aca gag gca gag gag ctg ttt ggg gag acc atg gag	3312
Gln Ser Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu Thr Met Glu	
1090 1095 1100	
atg atg gac agg atg aaa gac atg gag ttg gag ctg ctg cgg ggc agc	3360
Met Met Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu Arg Gly Ser	
1105 1110 1115 1120	
cag gcc atc atg ctg cgc tca gcg gac ctg aca gga ctg gag aag cgt	3408
Gln Ala Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu Glu Lys Arg	
1125 1130 1135	
gtg gag cag atc cgt gac cac atc aat ggg cgc gtg ctc tac tat gcc	3456
Val Glu Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu Tyr Tyr Ala	
1140 1145 1150	
acc tgc aag tgat	3469
Thr Cys Lys	

1155

<210> 24

<211> 1155

<212> PRT

<213> Homo sapiens

<400> 24

Gln Gln Ala Cys Ser Arg Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu
1 5 10 15

Leu Val Gly Arg Thr Arg Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu
20 25 30

Thr Lys Pro Glu Thr Tyr Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys
35 40 45

Cys Cys Lys Cys Asp Ser Arg Gln Pro His Asn Tyr Tyr Ser His Arg
50 55 60

Val Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln Ser
65 70 75 80

Gln Asn Asp Val Asn Pro Val Ser Leu Gln Leu Asp Leu Asp Arg Arg
85 90 95

Phe Gln Leu Gln Glu Val Met Met Glu Phe Gln Gly Pro Met Pro Ala
100 105 110

Gly Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Arg Val
115 120 125

Tyr Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val Arg
130 135 140

Gln Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu Pro
145 150 155 160

Gln Arg Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn Leu
165 170 175

Met Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile Gln
180 185 190

Glu Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu Ala
195 200 205

Pro Val Pro Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala Val
210 215 220

Ser Gln Leu Arg Leu Gln Gly Ser Cys Phe Cys His Gly His Ala Asp
225 230 235 240

Arg Cys Ala Pro Lys Pro Gly Ala Ser Ala Gly Pro Ser Thr Ala Val
245 250 255

Gln Val His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro Asn
260 265 270

Cys Glu Arg Cys Ala Pro Phe Tyr Asn Asn Arg Pro Trp Arg Pro Ala

275	280	285
Glu Gly Gln Asp Ala His 290	Glu Cys Gln Arg Cys 295	Asp Cys Asn Gly His 300
Ser Glu Thr Cys His Phe 305	Asp Pro Ala Val Phe 310	Ala Ala Ser Gln Gly 315
Ala Tyr Gly Gly Val Cys 325	Asp Asn Cys Arg Asp 330	His Thr Glu Gly Lys 335
Asn Cys Glu Arg Cys Gln 340	Leu His Tyr Phe Arg 345	Asn Arg Arg Pro Gly 350
Ala Ser Ile Gln Glu Thr 355	Cys Ile Ser Cys Glu 360	Cys Asp Pro Asp Gly 365
Ala Val Pro Gly Ala Pro 370	Cys Asp Pro Val Thr 375	Gly Gln Cys Val Cys 380
Lys Glu His Val Gln Gly 385	Glu Arg Cys Asp Leu 390	Cys Lys Pro Gly Phe 395
Thr Gly Leu Thr Tyr Ala 405	Asn Pro Gln Gly Cys 410	His Arg Cys Asp Cys 415
Asn Ile Leu Gly Ser Arg 420	Arg Asp Met Pro Cys 425	Asp Glu Glu Ser Gly 430
Arg Cys Leu Cys Leu Pro 435	Asn Val Val Gly Pro 440	Lys Cys Asp Gln Cys 445
Ala Pro Tyr His Trp Lys 450	Leu Ala Ser Gly Gln 455	Gly Cys Glu Pro Cys 460
Ala Cys Asp Pro His Asn 465	Ser Leu Ser Pro Gln 470	Cys Asn Gln Phe Thr 475
Gly Gln Cys Pro Cys Arg 485	Glu Gly Phe Gly Gly 490	Leu Met Cys Ser Ala 495
Ala Ala Ile Arg Gln Cys 500	Pro Asp Arg Thr Tyr 505	Gly Asp Val Ala Thr 510
Gly Cys Arg Ala Cys Asp 515	Cys Asp Phe Arg Gly 520	Thr Glu Gly Pro Gly 525
Cys Asp Lys Ala Ser Gly 530	Arg Cys Leu Cys Arg 535	Pro Gly Leu Thr Gly 540
Pro Arg Cys Asp Gln Cys 545	Gln Arg Gly Tyr Cys 550	Asn Arg Tyr Pro Val 555
Cys Val Ala Cys His Pro 565	Cys Phe Gln Thr Tyr 570	Asp Ala Asp Leu Arg 575
Glu Gln Ala Leu Arg Phe 580	Gly Arg Leu Arg Asn 585	Ala Thr Ala Ser Leu 590
Trp Ser Gly Pro Gly Leu 595	Glu Asp Arg Gly Leu 600	Ala Ser Arg Ile Leu 605

Asp Ala Lys Ser Lys Ile Glu Gln Ile Arg Ala Val Leu Ser Ser Pro
610 615 620

Ala Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu Ser
625 630 635 640

Leu Arg Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu
645 650 655

Glu Thr Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe
660 665 670

Asn Gly Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys
675 680 685

Ile Ser Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu Ser Thr Ala
690 695 700

Tyr Glu Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser Arg
705 710 715 720

Leu Leu Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu Val
725 730 735

Arg Gln Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val Ala
740 745 750

Leu Arg Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe Asn
755 760 765

Lys Leu Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser Cys
770 775 780

Pro Gly Glu Leu Cys Pro Gln Asp Asn Gly Thr Ala Cys Gly Ser Arg
785 790 795 800

Cys Arg Gly Val Leu Pro Arg Ala Gly Gly Ala Phe Leu Met Ala Gly
805 810 815

Gln Val Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr
820 825 830

Arg Gln Met Ile Arg Ala Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser
835 840 845

Ser Ala Gln Arg Leu Glu Thr Gln Val Ser Ala Ser Arg Ser Gln Met
850 855 860

Glu Glu Asp Val Arg Arg Thr Arg Leu Leu Ile Gln Gln Val Arg Asp
865 870 875 880

Phe Leu Thr Asp Pro Asp Thr Asp Ala Ala Thr Ile Gln Glu Val Ser
885 890 895

Glu Ala Val Leu Ala Leu Trp Leu Pro Thr Asp Ser Ala Thr Val Leu
900 905 910

Gln Lys Met Asn Glu Ile Gln Ala Ile Ala Ala Arg Leu Pro Asn Val
915 920 925

Asp Leu Val Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg
930 935 940

Leu Gln Ala Glu Ala Glu Glu Ala Arg Ser Arg Ala His Ala Val Glu
945 950 955 960

Gly Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val Ala
965 970 975

Leu Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu Arg
980 985 990

Leu Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro Ala
995 1000 1005

Glu Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp Thr
1010 1015 1020

Arg Met Glu Glu Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu Ala
1025 1030 1035 1040

Val Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln Ala Leu Ser
1045 1050 1055

Ala Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys
1060 1065 1070

Asp Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg Ile
1075 1080 1085

Gln Ser Val Lys Thr Glu Ala Glu Glu Leu Phe Gly Glu Thr Met Glu
1090 1095 1100

Met Met Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu Arg Gly Ser
1105 1110 1115 1120

Gln Ala Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu Glu Lys Arg
1125 1130 1135

Val Glu Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu Tyr Tyr Ala
1140 1145 1150

Thr Cys Lys
1155

<210> 25

<211> 5200

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118)..(3696)

<220>

<221> sig_peptide

<222> (118)..(180)

<400> 25

gaccacctga tcgaaggaaa aggaaggcac agcggagcgc agagtgagaa ccaccaaccg 60

```

aggcgccggg cagcgacccc tgcagcggag acagagactg agcggcccgg caccgcc      117

atg cct gcg ctc tgg ctg ggc tgc tgc ctc tgc ttc tcg ctc ctc ctg      165
Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
  1           5           10           15

ccc gca gcc cgg gcc acc tcc agg agg gaa gtc tgt gat tgc aat ggg      213
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
          20           25           30

aag tcc agg cag tgt atc ttt gat cgg gaa ctt cac aga caa act ggt      261
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
          35           40           45

aat gga ttc cgc tgc ctc aac tgc aat gac aac act gat ggc att cac      309
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
          50           55           60

tgc gag aag tgc aag aat ggc ttt tac cgg cac aga gaa agg gac cgc      357
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
          65           70           75           80

tgt ttg ccc tgc aat tgt aac tcc aaa ggt tct ctt agt gct cga tgt      405
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
          85           90           95

gac aac tct gga cgg tgc agc tgt aaa cca ggt gtg aca gga gcc aga      453
Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
          100          105          110

tgc gac cga tgt ctg cca ggc ttc cac atg ctc acg gat gcg ggg tgc      501
Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
          115          120          125

acc caa gac cag aga ctg cta gac tcc aag tgt gac tgt gac cca gct      549
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
          130          135          140

ggc atc gca ggg ccc tgt gac gcg ggc cgc tgt gtc tgc aag cca gct      597
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
          145          150          155          160

gtt act gga gaa cgc tgt gat agg tgt cga tca ggt tac tat aat ctg      645
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
          165          170          175

gat ggg ggg aac cct gag ggc tgt acc cag tgt ttc tgc tat ggg cat      693
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
          180          185          190

tca gcc agc tgc cgc agc tct gca gaa tac agt gtc cat aag atc acc      741
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
          195          200          205

tct acc ttt cat caa gat gtt gat ggc tgg aag gct gtc caa cga aat      789
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
          210          215          220

ggg tct cct gca aag ctc caa tgg tca cag cgc cat caa gat gtg ttt      837
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Ph

```

225	230	235	240	
agc tca gcc caa cga cta gat cct gtc tat ttt gtg gct cct gcc aaa				885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys				
	245	250	255	
ttt ctt ggg aat caa cag gtg agc tat ggg caa agc ctg tcc ttt gac				933
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp				
	260	265	270	
tac cgt gtg gac aga gga ggc aga cac cca tct gcc cat gat gtg atc				981
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile				
	275	280	285	
ctg gaa ggt gct ggt cta cgg atc aca gct ccc ttg atg cca ctt ggc				1029
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly				
	290	295	300	
aag aca ctg cct tgt ggg ctc acc aag act tac aca ttc agg tta aat				1077
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn				
	305	310	315	320
gag cat cca agc aat aat tgg agc ccc cag ctg agt tac ttt gag tat				1125
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr				
	325	330	335	
cga agg tta ctg cgg aat ctc aca gcc ctc cgc atc cga gct aca tat				1173
Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr				
	340	345	350	
gga gaa tac agt act ggg tac att gac aat gtg acc ctg att tca gcc				1221
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala				
	355	360	365	
cgc cct gtc tct gga gcc cca gca ccc tgg gtt gaa cag tgt ata tgt				1269
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys				
	370	375	380	
cct gtt ggg tac aag ggg caa ttc tgc cag gat tgt gct tct ggc tac				1317
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr				
	385	390	395	400
aag aga gat tca gcg aga ctg ggg cct ttt ggc acc tgt att cct tgt				1365
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys				
	405	410	415	
aac tgt caa ggg gga ggg gcc tgt gat cca gac aca gga gat tgt tat				1413
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr				
	420	425	430	
tca ggg gat gag aat cct gac att gag tgt gct gac tgc cca att ggt				1461
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly				
	435	440	445	
ttc tac aac gat ccg cac gac ccc cgc agc tgc aag cca tgt ccc tgt				1509
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys				
	450	455	460	
cat aac ggg ttc agc tgc tca gtg att ccg gag acg gag gag gtg gtg				1557
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val				
	465	470	475	480

tgc aat aac tgc cct ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt	1605
Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys	
485 490 495	
gct gat ggc tac ttt ggg gac ccc ttt ggt gaa cat ggc cca gtg agg	1653
Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg	
500 505 510	
cct tgt cag ccc tgt caa tgc aac agc aat gtg gac ccc agt gcc tct	1701
Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser	
515 520 525	
ggg aat tgt gac cgg ctg aca ggc agg tgt ttg aag tgt atc cac aac	1749
Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn	
530 535 540	
aca gcc ggc atc tac tgc gac cag tgc aaa gca ggc tac ttc ggg gac	1797
Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp	
545 550 555 560	
cca ttg gct ccc aac cca gca gac aag tgt cga gct tgc aac tgt aac	1845
Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn	
565 570 575	
ccc atg ggc tca gag cct gta gga tgt cga agt gat ggc acc tgt gtt	1893
Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val	
580 585 590	
tgc aag cca gga ttt ggt ggc ccc aac tgt gag cat gga gca ttc agc	1941
Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser	
595 600 605	
tgt cca gct tgc tat aat caa gtg aag att cag atg gat cag ttt atg	1989
Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met	
610 615 620	
cag cag ctt cag aga atg gag gcc ctg att tca aag gct cag ggt ggt	2037
Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly	
625 630 635 640	
gat gga gta gta cct gat aca gag ctg gaa ggc agg atg cag cag gct	2085
Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala	
645 650 655	
gag cag gcc ctt cag gac att ctg aga gat gcc cag att tca gaa ggt	2133
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly	
660 665 670	
gct agc aga tcc ctt ggt ctc cag ttg gcc aag gtg agg agc caa gag	2181
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu	
675 680 685	
aac agc tac cag agc cgc ctg gat gac ctc aag atg act gtg gaa aga	2229
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg	
690 695 700	
gtt cgg gct ctg gga agt cag tac cag aac cga gtt cgg gat act cac	2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His	
705 710 715 720	

agg ctc atc act cag atg cag ctg agc ctg gca gaa agt gaa gct tcc	2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser	
725 730 735	
ttg gga aac act aac att cct gcc tca gac cac tac gtg ggg cca aat	2373
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn	
740 745 750	
ggc ttt aaa agt ctg gct cag gag gcc aca aga tta gca gaa agc cac	2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His	
755 760 765	
gtt gag tca gcc agt aac atg gag caa ctg aca agg gaa act gag gac	2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp	
770 775 780	
tat tcc aaa caa gcc ctc tca ctg gtg cgc aag gcc ctg cat gaa gga	2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly	
785 790 795 800	
gtc gga agc gga agc ggt agc ccg gac ggt gct gtg gtg caa ggg ctt	2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu	
805 810 815	
gtg gaa aaa ttg gag aaa acc aag tcc ctg gcc cag cag ttg aca agg	2613
Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg	
820 825 830	
gag gcc act caa gcg gaa att gaa gca gat agg tct tat cag cac agt	2661
Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser	
835 840 845	
ctc cgc ctc ctg gat tca gtg tct ccg ctt cag gga gtc agt gat cag	2709
Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln	
850 855 860	
tcc ttt cag gtg gaa gaa gca aag agg atc aaa caa aaa gcg gat tca	2757
Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser	
865 870 875 880	
ctc tca agc ctg gta acc agg cat atg gat gag ttc aag cgt aca caa	2805
Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln	
885 890 895	
aag aat ctg gga aac tgg aaa gaa gaa gca cag cag ctc tta cag aat	2853
Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn	
900 905 910	
gga aaa agt ggg aga gag aaa tca gat cag ctg ctt tcc cgt gcc aat	2901
Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn	
915 920 925	
ctt gct aaa agc aga gca caa gaa gca ctg agt atg ggc aat gcc act	2949
Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr	
930 935 940	
ttt tat gaa gtt gag agc atc ctt aaa aac ctc aga gag ttt gac ctg	2997
Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu	
945 950 955 960	
cag gtg gac aac aga aaa gca gaa gct gaa gaa gcc atg aag aga ctc	3045

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu	
965 970 975	
tcc tac atc agc cag aag gtt tca gat gcc agt gac aag acc cag caa	3093
Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln	
980 985 990	
gca gaa aga gcc ctg ggg agc gct gct gct gat gca cag agg gca aag	3141
Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys	
995 1000 1005	
aat ggg gcc ggg gag gcc ctg gaa atc tcc agt gag att gaa cag gag	3189
Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu	
1010 1015 1020	
att ggg agt ctg aac ttg gaa gcc aat gtg aca gca gat gga gcc ttg	3237
Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu	
1025 1030 1035 1040	
gcc atg gaa aag gga ctg gcc tct ctg aag agt gag atg agg gaa gtg	3285
Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val	
1045 1050 1055	
gaa gga gag ctg gaa agg aag gag ctg gag ttt gac acg aat atg gat	3333
Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp	
1060 1065 1070	
gca gta cag atg gtg att aca gaa gcc cag aag gtt gat acc aga gcc	3381
Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala	
1075 1080 1085	
aag aac gct ggg gtt aca atc caa gac aca ctc aac aca tta gac ggc	3429
Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly	
1090 1095 1100	
ctc ctg cat ctg atg gac cag cct ctc agt gta gat gaa gag ggg ctg	3477
Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu	
1105 1110 1115 1120	
gtc tta ctg gag cag aag ctt tcc cga gcc aag acc cag atc aac agc	3525
Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser	
1125 1130 1135	
caa ctg cgg ccc atg atg tca gag ctg gaa gag agg gca cgt cag cag	3573
Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln	
1140 1145 1150	
agg ggc cac ctc cat ttg ctg gag aca agc ata gat ggg att ctg gct	3621
Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala	
1155 1160 1165	
gat gtg aag aac ttg gag aac att agg gac aac ctg ccc cca ggc tgc	3669
Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys	
1170 1175 1180	
tac aat acc cag gct ctt gag caa cag tgaagctgcc ataaatattt	3716
Tyr Asn Thr Gln Ala Leu Glu Gln Gln	
1185 1190	
ctcaactgag gttcttgga tacagatctc agggctcggg agccatgtca tgtgagtggg	3776

tgggatgggg acatttgaac atgtttaatg ggtatgctca ggtcaactga cctgacccca 3836
 ttcttgatcc catggccagg tggttgtctt attgcaccat actccttgct tcctgatgct 3896
 gggcatgagg cagataggca ctggtgtgag aatgatcaag gatctggacc ccaaagatag 3956
 actggatgga aagacaaact gcacaggcag atgtttgcct cataatagtc gtaagtggag 4016
 tcctggaatt tggacaagtg ctgttgggat atagtcaact tattctttga gtaatgtgac 4076
 taaaggaaaa aactttgact ttgcccaggc atgaaattct tcctaattgtc agaacagagt 4136
 gcaacccagt cacactgtgg ccagtaaaat actattgcct catattgtcc tctgcaagct 4196
 tcttgctgat cagagttcct cctacttaca acccaggggtg tgaacatgtt ctccattttc 4256
 aagctggaag aagtgagcag tgttggagtg aggacctgta aggcaggccc attcagagct 4316
 atggtgcttg ctggtgcctg ccaccttcaa gttctggacc tgggcatgac atcctttctt 4376
 ttaatgatgc catggcaact tagagattgc atttttatta aagcatttcc taccagcaaa 4436
 gcaaattgttg ggaaagtatt tactttttcg gtttcaaagt gatagaaaag tgtggcttgg 4496
 gcattgaaag aggtaaaatt ctctagattt attagtccta attcaatcct acttttcgaa 4556
 caccaaaaat gatgcgcac aatgtatttt atcttatttt ctcaatctcc tctctctttc 4616
 ctccacccat aataagagaa tgttcctact cacacttcag ctgggtcaca tccatccctc 4676
 cattcatcct tccatccatc tttccatcca ttacctccat ccacccctcc aacatatatt 4736
 tattgagtac ctactgtgtg ccaggggctg gtgggacagt ggtgacatag tctctgccct 4796
 catagagtthg attgtctagt gaggaagaca agcattttta aaaaataaat ttaaacttac 4856
 aaactttggt tgtcacaagt ggtgtttatt gcaataaccg cttgggtttgc aacctctttg 4916
 ctcaacagaa catatgttgc aagacctcc catgggcact gagtttggca aggatgacag 4976
 agctctgggt tgtgcacatt tctttgcatt ccagcgtcac tctgtgcctt ctacaactga 5036
 ttgcaacaga ctgttgagtt atgataacac cagtgggaat tgctggagga accagaggca 5096
 cttccacctt ggctgggaag actatgggtgc tgccttgctt ctgtatttcc ttggattttc 5156
 ctgaaagtgt ttttaaataa agaacaattg ttagatgcc aaaa 5200

<210> 26

<211> 1193

<212> PRT

<213> Homo sapiens

<400> 26

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
 1 5 10 15

Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
 20 25 30

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
35 40 45

Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
50 55 60

Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
65 70 75 80

Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
85 90 95

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
100 105 110

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
115 120 125

Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
130 135 140

Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145 150 155 160

Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
165 170 175

Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
180 185 190

Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
195 200 205

Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
210 215 220

Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225 230 235 240

Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
245 250 255

Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
260 265 270

Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
275 280 285

Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
290 295 300

Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305 310 315 320

Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
325 330 335

Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
340 345 350

Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala

355 360 365

Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
370 375 380

Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385 390 395 400

Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
405 410 415

Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
420 425 430

Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
435 440 445

Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
450 455 460

His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465 470 475 480

Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
485 490 495

Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
500 505 510

Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
515 520 525

Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
530 535 540

Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545 550 555 560

Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
565 570 575

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
580 585 590

Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
595 600 605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
610 615 620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625 630 635 640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
645 650 655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
660 665 670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
675 680 685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
690 695 700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705 710 715 720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
725 730 735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
740 745 750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
755 760 765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
770 775 780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785 790 795 800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
805 810 815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
820 825 830

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
835 840 845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
850 855 860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865 870 875 880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
885 890 895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
900 905 910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
915 920 925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
930 935 940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945 950 955 960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
965 970 975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
980 985 990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
995 1000 1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu
 1010 1015 1020

Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu
 1025 1030 1035 1040

Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val
 1045 1050 1055

Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp
 1060 1065 1070

Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala
 1075 1080 1085

Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly
 1090 1095 1100

Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu
 1105 1110 1115 1120

Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser
 1125 1130 1135

Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln
 1140 1145 1150

Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala
 1155 1160 1165

Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys
 1170 1175 1180

Tyr Asn Thr Gln Ala Leu Glu Gln Gln
 1185 1190

<210> 27

<211> 5020

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (3516)

<400> 27

acc tcc agg agg gaa gtc tgt gat tgc aat ggg aag tcc agg cag tgt 48
 Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys
 1 5 10 15

atc ttt gat cgg gaa ctt cac aga caa act ggt aat gga ttc cgc tgc 96
 Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly Asn Gly Phe Arg Cys
 20 25 30

ctc aac tgc aat gac aac act gat ggc att cac tgc gag aag tgc aag 144
 Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His Cys Glu Lys Cys Lys
 35 40 45

aat ggc ttt tac cgg cac aga gaa agg gac cgc tgt ttg ccc tgc aat 192
 Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg Cys Leu Pro Cys Asn

50	55	60	
tgt aac tcc aaa ggt tct ctt agt gct cga tgt gac aac tct gga cgg			240
Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys Asp Asn Ser Gly Arg			
65	70	75	80
tgc agc tgt aaa cca ggt gtg aca gga gcc aga tgc gac cga tgt ctg			288
Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg Cys Asp Arg Cys Leu			
	85	90	95
cca ggc ttc cac atg ctc acg gat gcg ggg tgc acc caa gac cag aga			336
Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys Thr Gln Asp Gln Arg			
	100	105	110
ctg cta gac tcc aag tgt gac tgt gac cca gct ggc atc gca ggg ccc			384
Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala Gly Ile Ala Gly Pro			
	115	120	125
tgt gac gcg ggc cgc tgt gtc tgc aag cca gct gtt act gga gaa cgc			432
Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala Val Thr Gly Glu Arg			
	130	135	140
tgt gat agg tgt cga tca ggt tac tat aat ctg gat ggg ggg aac cct			480
Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu Asp Gly Gly Asn Pro			
	145	150	155
gag ggc tgt acc cag tgt ttc tgc tat ggg cat tca gcc agc tgc cgc			528
Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His Ser Ala Ser Cys Arg			
	165	170	175
agc tct gca gaa tac agt gtc cat aag atc acc tct acc ttt cat caa			576
Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr Ser Thr Phe His Gln			
	180	185	190
gat gtt gat ggc tgg aag gct gtc caa cga aat ggg tct cct gca aag			624
Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn Gly Ser Pro Ala Lys			
	195	200	205
ctc caa tgg tca cag cgc cat caa gat gtg ttt agc tca gcc caa cga			672
Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe Ser Ser Ala Gln Arg			
	210	215	220
cta gat cct gtc tat ttt gtg gct cct gcc aaa ttt ctt ggg aat caa			720
Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys Phe Leu Gly Asn Gln			
	225	230	235
cag gtg agc tat ggg caa agc ctg tcc ttt gac tac cgt gtg gac aga			768
Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp Tyr Arg Val Asp Arg			
	245	250	255
gga ggc aga cac cca tct gcc cat gat gtg atc ctg gaa ggt gct ggt			816
Gly Gly Arg His Pro Ser Ala His Asp Val Ile Leu Glu Gly Ala Gly			
	260	265	270
cta cgg atc aca gct ccc ttg atg cca ctt ggc aag aca ctg cct tgt			864
Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly Lys Thr Leu Pro Cys			
	275	280	285
ggg ctc acc aag act tac aca ttc agg tta aat gag cat cca agc aat			912
Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn Glu His Pro Ser Asn			
	290	295	300

aat tgg agc ccc cag ctg agt tac ttt gag tat cga agg tta ctg cgg	960
Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr Arg Arg Leu Leu Arg	
305 310 315 320	
aat ctc aca gcc ctc cgc atc cga gct aca tat gga gaa tac agt act	1008
Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr Gly Glu Tyr Ser Thr	
325 330 335	
ggg tac att gac aat gtg acc ctg att tca gcc cgc cct gtc tct gga	1056
Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala Arg Pro Val Ser Gly	
340 345 350	
gcc cca gca ccc tgg gtt gaa cag tgt ata tgt cct gtt ggg tac aag	1104
Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys Pro Val Gly Tyr Lys	
355 360 365	
ggg caa ttc tgc cag gat tgt gct tct ggc tac aag aga gat tca gcg	1152
Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala	
370 375 380	
aga ctg ggg cct ttt ggc acc tgt att cct tgt aac tgt caa ggg gga	1200
Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly	
385 390 395 400	
ggg gcc tgt gat cca gac aca gga gat tgt tat tca ggg gat gag aat	1248
Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn	
405 410 415	
cct gac att gag tgt gct gac tgc cca att ggt ttc tac aac gat ccg	1296
Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro	
420 425 430	
cac gac ccc cgc agc tgc aag cca tgt ccc tgt cat aac ggg ttc agc	1344
His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser	
435 440 445	
tgc tca gtg att ccg gag acg gag gag gtg gtg tgc aat aac tgc cct	1392
Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro	
450 455 460	
ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt gct gat ggc tac ttt	1440
Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe	
465 470 475 480	
ggg gac ccc ttt ggt gaa cat ggc cca gtg agg cct tgt cag ccc tgt	1488
Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys	
485 490 495	
caa tgc aac agc aat gtg gac ccc agt gcc tct ggg aat tgt gac cgg	1536
Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg	
500 505 510	
ctg aca ggc agg tgt ttg aag tgt atc cac aac aca gcc ggc atc tac	1584
Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr	
515 520 525	
tgc gac cag tgc aaa gca ggc tac ttc ggg gac cca ttg gct ccc aac	1632
Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn	
530 535 540	

cca gca gac aag tgt cga gct tgc aac tgt aac ccc atg ggc tca gag	1680
Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu	
545 550 555 560	
cct gta gga tgt cga agt gat ggc acc tgt gtt tgc aag cca gga ttt	1728
Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe	
565 570 575	
ggc ggc ccc aac tgt gag cat gga gca ttc agc tgt cca gct tgc tat	1776
Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser Cys Pro Ala Cys Tyr	
580 585 590	
aat caa gtg aag att cag atg gat cag ttt atg cag cag ctt cag aga	1824
Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met Gln Gln Leu Gln Arg	
595 600 605	
atg gag gcc ctg att tca aag gct cag ggt ggt gat gga gta gta cct	1872
Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly Asp Gly Val Val Pro	
610 615 620	
gat aca gag ctg gaa ggc agg atg cag cag gct gag cag gcc ctt cag	1920
Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala Glu Gln Ala Leu Gln	
625 630 635 640	
gac att ctg aga gat gcc cag att tca gaa ggt gct agc aga tcc ctt	1968
Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly Ala Ser Arg Ser Leu	
645 650 655	
ggc ctc cag ttg gcc aag gtg agg agc caa gag aac agc tac cag agc	2016
Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu Asn Ser Tyr Gln Ser	
660 665 670	
cgc ctg gat gac ctc aag atg act gtg gaa aga gtt cgg gct ctg gga	2064
Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg Val Arg Ala Leu Gly	
675 680 685	
agt cag tac cag aac cga gtt cgg gat act cac agg ctc atc act cag	2112
Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His Arg Leu Ile Thr Gln	
690 695 700	
atg cag ctg agc ctg gca gaa agt gaa gct tcc ttg gga aac act aac	2160
Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser Leu Gly Asn Thr Asn	
705 710 715 720	
att cct gcc tca gac cac tac gtg ggg cca aat ggc ttt aaa agt ctg	2208
Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn Gly Phe Lys Ser Leu	
725 730 735	
gct cag gag gcc aca aga tta gca gaa agc cac gtt gag tca gcc agt	2256
Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His Val Glu Ser Ala Ser	
740 745 750	
aac atg gag caa ctg aca agg gaa act gag gac tat tcc aaa caa gcc	2304
Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp Tyr Ser Lys Gln Ala	
755 760 765	
ctc tca ctg gtg cgc aag gcc ctg cat gaa gga gtc gga agc gga agc	2352
Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly Val Gly Ser Gly Ser	
770 775 780	
ggc agc ccg gac ggt gct gtg gtg caa ggg ctt gtg gaa aaa ttg gag	2400

Gly 785	Ser	Pro	Asp	Gly	Ala 790	Val	Val	Gln	Gly	Leu 795	Val	Glu	Lys	Leu	Glu 800	
aaa	acc	aag	tcc	ctg	gcc	cag	cag	ttg	aca	agg	gag	gcc	act	caa	gcg	2448
Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg	Glu	Ala	Thr	Gln	Ala	
				805				810						815		
gaa	att	gaa	gca	gat	agg	tct	tat	cag	cac	agt	ctc	cgc	ctc	ctg	gat	2496
Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser	Leu	Arg	Leu	Leu	Asp	
			820					825					830			
tca	gtg	tct	ccg	ctt	cag	gga	gtc	agt	gat	cag	tcc	ttt	cag	gtg	gaa	2544
Ser	Val	Ser	Pro	Leu	Gln	Gly	Val	Ser	Asp	Gln	Ser	Phe	Gln	Val	Glu	
		835					840					845				
gaa	gca	aag	agg	atc	aaa	caa	aaa	gcg	gat	tca	ctc	tca	agc	ctg	gta	2592
Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser	Leu	Ser	Ser	Leu	Val	
	850					855					860					
acc	agg	cat	atg	gat	gag	ttc	aag	cgt	aca	caa	aag	aat	ctg	gga	aac	2640
Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln	Lys	Asn	Leu	Gly	Asn	
865					870					875					880	
tgg	aaa	gaa	gaa	gca	cag	cag	ctc	tta	cag	aat	gga	aaa	agt	ggg	aga	2688
Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn	Gly	Lys	Ser	Gly	Arg	
				885					890					895		
gag	aaa	tca	gat	cag	ctg	ctt	tcc	cgt	gcc	aat	ctt	gct	aaa	agc	aga	2736
Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn	Leu	Ala	Lys	Ser	Arg	
			900					905					910			
gca	caa	gaa	gca	ctg	agt	atg	ggc	aat	gcc	act	ttt	tat	gaa	gtt	gag	2784
Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr	Phe	Tyr	Glu	Val	Glu	
	915						920				925					
agc	atc	ctt	aaa	aac	ctc	aga	gag	ttt	gac	ctg	cag	gtg	gac	aac	aga	2832
Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu	Gln	Val	Asp	Asn	Arg	
	930					935					940					
aaa	gca	gaa	gct	gaa	gaa	gcc	atg	aag	aga	ctc	tcc	tac	atc	agc	cag	2880
Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu	Ser	Tyr	Ile	Ser	Gln	
945						950				955					960	
aag	gtt	tca	gat	gcc	agt	gac	aag	acc	cag	caa	gca	gaa	aga	gcc	ctg	2928
Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln	Ala	Glu	Arg	Ala	Leu	
				965					970					975		
ggg	agc	gct	gct	gct	gat	gca	cag	agg	gca	aag	aat	ggg	gcc	ggg	gag	2976
Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys	Asn	Gly	Ala	Gly	Glu	
			980					985				990				
gcc	ctg	gaa	atc	tcc	agt	gag	att	gaa	cag	gag	att	ggg	agt	ctg	aac	3024
Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu	Ile	Gly	Ser	Leu	Asn	
		995				1000					1005					
ttg	gaa	gcc	aat	gtg	aca	gca	gat	gga	gcc	ttg	gcc	atg	gaa	aag	gga	3072
Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu	Ala	Met	Glu	Lys	Gly	
	1010					1015				1020						
ctg	gcc	tct	ctg	aag	agt	gag	atg	agg	gaa	gtg	gaa	gga	gag	ctg	gaa	3120
Leu	Ala	Ser	Leu	Lys	Ser	Glu	Met	Arg	Glu	Val	Glu	Gly	Glu	Leu	Glu	

1025 1030 1035 1040
agg aag gag ctg gag ttt gac acg aat atg gat gca gta cag atg gtg 3168
Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp Ala Val Gln Met Val
1045 1050 1055
att aca gaa gcc cag aag gtt gat acc aga gcc aag aac gct ggg gtt 3216
Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala Lys Asn Ala Gly Val
1060 1065 1070
aca atc caa gac aca ctc aac aca tta gac ggc ctc ctg cat ctg atg 3264
Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met
1075 1080 1085
gac cag cct ctc agt gta gat gaa gag ggg ctg gtc tta ctg gag cag 3312
Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln
1090 1095 1100
aag ctt tcc cga gcc aag acc cag atc aac agc caa ctg cgg ccc atg 3360
Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met
1105 1110 1115 1120
atg tca gag ctg gaa gag agg gca cgt cag cag agg ggc cac ctc cat 3408
Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His
1125 1130 1135
ttg ctg gag aca agc ata gat ggg att ctg gct gat gtg aag aac ttg 3456
Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu
1140 1145 1150
gag aac att agg gac aac ctg ccc cca ggc tgc tac aat acc cag gct 3504
Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln Ala
1155 1160 1165
ctt gag caa cag tgaagctgcc ataatatatt ctcaactgag gttcttgga 3556
Leu Glu Gln Gln
1170
tacagatctc agggctcggg agccatgtca tgtgagtggg tgggatgggg acatttgaac 3616
atgtttaatg ggtatgctca ggtcaactga cctgaccca ttctgatcc catggccagg 3676
tggttgcttt attgcacat actccttgct tctgatgct gggcatgagg cagataggca 3736
ctggtgtgag aatgatcaag gatctggacc ccaaagatag actggatgga aagacaaact 3796
gcacaggcag atgtttgcct cataatagtc gtaagtggag tcttgggaatt tggacaagtg 3856
ctgttgggat atagtcaact tattctttga gtaatgtgac taaaggaaaa aactttgact 3916
ttgcccaggc atgaaattct tctaatgtc agaacagagt gcaaccagc cacactgtgg 3976
ccagtaaaat actattgcct catattgtcc tctgcaagct tcttgctgat cagagttcct 4036
cctacttaca acccaggggtg tgaacatgtt ctccattttc aagctggaag aagtgagcag 4096
tggttgagtg aggacctgta aggcaggccc attcagagct atggtgcttg ctggtgcctg 4156
ccaccttcaa gttctggacc tgggcatgac atcctttctt ttaatgatgc catggcaact 4216
tagagattgc atttttatta aagcatttcc taccagcaaa gcaaatgttg ggaaagtatt 4276

tacttttttcg gtttcaaagt gatagaaaag tgtggcttgg gcattgaaag aggtaaaatt 4336
 ctctagattt attagtccta attcaatcct acttttcgaa caccaaaaat gatgcgcac 4396
 aatgtatttt atcttatttt ctcaatctcc tctctctttc ctccacccat aataagagaa 4456
 tgttcctact cacacttcag ctgggtcaca tccatccctc cattcatcct tccatccatc 4516
 ttcccatcca ttacctccat ccacctctcc aacatatatt tattgagtac ctactgtgtg 4576
 ccaggggctg gtgggacagt ggtgacatag tctctgccct catagagttg attgtctagt 4636
 gaggaagaca agcattttta aaaaataaat ttaaacttac aaactttggt tgtcacaagt 4696
 ggtgtttatt gcaataaccg cttggtttgc aacctctttg ctcaacagaa catatgttgc 4756
 aagaccctcc catgggcact gagtttggca aggatgacag agctctgggt tgtgcacatt 4816
 tctttgcatt ccagcgtcac tctgtgcctt ctacaactga ttgcaacaga ctgttgagtt 4876
 atgataacac cagtgggaat tgctggagga accagaggca ctccacctt ggctgggaag 4936
 actatggtgc tgccttgctt ctgtatttcc ttggattttc ctgaaagtgt ttttaaataa 4996
 agaacaattg ttagatgcca aaaa 5020

<210> 28

<211> 1172

<212> PRT

<213> Homo sapiens

<400> 28

Thr	Ser	Arg	Arg	Glu	Val	Cys	Asp	Cys	Asn	Gly	Lys	Ser	Arg	Gln	Cys
1				5					10					15	
Ile	Phe	Asp	Arg	Glu	Leu	His	Arg	Gln	Thr	Gly	Asn	Gly	Phe	Arg	Cys
			20					25					30		
Leu	Asn	Cys	Asn	Asp	Asn	Thr	Asp	Gly	Ile	His	Cys	Glu	Lys	Cys	Lys
		35					40					45			
Asn	Gly	Phe	Tyr	Arg	His	Arg	Glu	Arg	Asp	Arg	Cys	Leu	Pro	Cys	Asn
	50				55						60				
Cys	Asn	Ser	Lys	Gly	Ser	Leu	Ser	Ala	Arg	Cys	Asp	Asn	Ser	Gly	Arg
65					70				75					80	
Cys	Ser	Cys	Lys	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Asp	Arg	Cys	Leu
			85					90						95	
Pro	Gly	Phe	His	Met	Leu	Thr	Asp	Ala	Gly	Cys	Thr	Gln	Asp	Gln	Arg
		100						105					110		
Leu	Leu	Asp	Ser	Lys	Cys	Asp	Cys	Asp	Pro	Ala	Gly	Ile	Ala	Gly	Pro
		115					120					125			
Cys	Asp	Ala	Gly	Arg	Cys	Val	Cys	Lys	Pro	Ala	Val	Thr	Gly	Glu	Arg
130						135						140			

Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu Asp Gly Gly Asn Pro
145 150 155 160

Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His Ser Ala Ser Cys Arg
165 170 175

Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr Ser Thr Phe His Gln
180 185 190

Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn Gly Ser Pro Ala Lys
195 200 205

Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe Ser Ser Ala Gln Arg
210 215 220

Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys Phe Leu Gly Asn Gln
225 230 235 240

Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp Tyr Arg Val Asp Arg
245 250 255

Gly Gly Arg His Pro Ser Ala His Asp Val Ile Leu Glu Gly Ala Gly
260 265 270

Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly Lys Thr Leu Pro Cys
275 280 285

Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn Glu His Pro Ser Asn
290 295 300

Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr Arg Arg Leu Leu Arg
305 310 315 320

Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr Gly Glu Tyr Ser Thr
325 330 335

Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala Arg Pro Val Ser Gly
340 345 350

Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys Pro Val Gly Tyr Lys
355 360 365

Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala
370 375 380

Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly
385 390 395 400

Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn
405 410 415

Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro
420 425 430

His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser
435 440 445

Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro
450 455 460

Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe

465		470		475		480
Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys						
	485			490		495
Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg						
	500			505		510
Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr						
	515			520		525
Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn						
	530			535		540
Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu						
	545			550		555
Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe						
	565			570		575
Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser Cys Pro Ala Cys Tyr						
	580			585		590
Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met Gln Gln Leu Gln Arg						
	595			600		605
Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly Asp Gly Val Val Pro						
	610			615		620
Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala Glu Gln Ala Leu Gln						
	625			630		635
Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly Ala Ser Arg Ser Leu						
	645			650		655
Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu Asn Ser Tyr Gln Ser						
	660			665		670
Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg Val Arg Ala Leu Gly						
	675			680		685
Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His Arg Leu Ile Thr Gln						
	690			695		700
Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser Leu Gly Asn Thr Asn						
	705			710		715
Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn Gly Phe Lys Ser Leu						
	725			730		735
Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His Val Glu Ser Ala Ser						
	740			745		750
Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp Tyr Ser Lys Gln Ala						
	755			760		765
Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly Val Gly Ser Gly Ser						
	770			775		780
Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu Val Glu Lys Leu Glu						
	785			790		795
						800

Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg Glu Ala Thr Gln Ala
805 810 815

Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser Leu Arg Leu Leu Asp
820 825 830

Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln Ser Phe Gln Val Glu
835 840 845

Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser Leu Ser Ser Leu Val
850 855 860

Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln Lys Asn Leu Gly Asn
865 870 875 880

Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn Gly Lys Ser Gly Arg
885 890 895

Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn Leu Ala Lys Ser Arg
900 905 910

Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr Phe Tyr Glu Val Glu
915 920 925

Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu Gln Val Asp Asn Arg
930 935 940

Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu Ser Tyr Ile Ser Gln
945 950 955 960

Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln Ala Glu Arg Ala Leu
965 970 975

Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys Asn Gly Ala Gly Glu
980 985 990

Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu Ile Gly Ser Leu Asn
995 1000 1005

Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu Ala Met Glu Lys Gly
1010 1015 1020

Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val Glu Gly Glu Leu Glu
1025 1030 1035 1040

Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp Ala Val Gln Met Val
1045 1050 1055

Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala Lys Asn Ala Gly Val
1060 1065 1070

Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met
1075 1080 1085

Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln
1090 1095 1100

Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met
1105 1110 1115 1120

Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His
 1125 1130 1135

Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu
 1140 1145 1150

Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln Ala
 1155 1160 1165

Leu Glu Gln Gln
 1170

<210> 29
 <211> 3720
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (38)..(3616)

<220>
 <221> sig_peptide
 <222> (38)..(100)

<400> 29
 gtttaaactt aagcttggtta ccgagctcgg atccgcc atg cct gcg ctc tgg ctg 55
 Met Pro Ala Leu Trp Leu
 1 5

ggc tgc tgc ctc tgc ttc tcg ctc ctc ctg ccc gca gcc cgg gcc acc 103
 Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu Pro Ala Ala Arg Ala Thr
 10 15 20

tcc agg agg gaa gtc tgt gat tgc aat ggg aag tcc agg cag tgt atc 151
 Ser Arg Arg Glu Val Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys Ile
 25 30 35

ttt gat cgg gaa ctt cac aga caa act ggt aat gga ttc cgc tgc ctc 199
 Phe Asp Arg Glu Leu His Arg Gln Thr Gly Asn Gly Phe Arg Cys Leu
 40 45 50

aac tgc aat gac aac act gat ggc att cac tgc gag aag tgc aag aat 247
 Asn Cys Asn Asp Asn Thr Asp Gly Ile His Cys Glu Lys Cys Lys Asn
 55 60 65 70

ggc ttt tac cgg cac aga gaa agg gac cgc tgt ttg ccc tgc aat tgt 295
 Gly Phe Tyr Arg His Arg Glu Arg Asp Arg Cys Leu Pro Cys Asn Cys
 75 80 85

aac tcc aaa ggt tct ctt agt gct cga tgt gac aac tct gga cgg tgc 343
 Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys Asp Asn Ser Gly Arg Cys
 90 95 100

agc tgt aaa cca ggt gtg aca gga gcc aga tgc gac cga tgt ctg cca 391
 Ser Cys Lys Pro Gly Val Thr Gly Ala Arg Cys Asp Arg Cys Leu Pro
 105 110 115

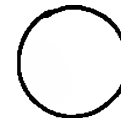
ggc ttc cac atg ctc acg gat gcg ggg tgc acc caa gac cag aga ctg 439
 Gly Phe His Met Leu Thr Asp Ala Gly Cys Thr Gln Asp Gln Arg Leu

120	125	130	
cta gac tcc aag tgt gac tgt gac cca gct ggc atc gca ggg ccc tgt			487
Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala Gly Ile Ala Gly Pro Cys			
135	140	145	150
gac gcg ggc cgc tgt gtc tgc aag cca gct gtt act gga gaa cgc tgt			535
Asp Ala Gly Arg Cys Val Cys Lys Pro Ala Val Thr Gly Glu Arg Cys			
	155	160	165
gat ggg tgt cga tca ggt tac tat aat ctg gat ggg ggg aac cct gag			583
Asp Gly Cys Arg Ser Gly Tyr Tyr Asn Leu Asp Gly Gly Asn Pro Glu			
	170	175	180
ggc tgt acc cag tgt ttc tgc tat ggg cat tca gcc agc tgc cgc agc			631
Gly Cys Thr Gln Cys Phe Cys Tyr Gly His Ser Ala Ser Cys Arg Ser			
	185	190	195
tct gca gaa tac agt gtc cat aag atc acc tct acc ttt cat caa gat			679
Ser Ala Glu Tyr Ser Val His Lys Ile Thr Ser Thr Phe His Gln Asp			
	200	205	210
gtt gat ggc tgg aag gct gtc caa cga aat ggg tct cct gca aag ctc			727
Val Asp Gly Trp Lys Ala Val Gln Arg Asn Gly Ser Pro Ala Lys Leu			
	215	220	230
caa tgg tca cag cgc cat caa gat gtg ttt agc tca gcc caa cga cta			775
Gln Trp Ser Gln Arg His Gln Asp Val Phe Ser Ser Ala Gln Arg Leu			
	235	240	245
gac cct gtc tat ttt gtg gct cct gcc aaa ttt ctt ggg aat caa cag			823
Asp Pro Val Tyr Phe Val Ala Pro Ala Lys Phe Leu Gly Asn Gln Gln			
	250	255	260
gtg agc tat ggg caa agc ctg tcc ttt gac tac cgt gtg gac aga gga			871
Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp Tyr Arg Val Asp Arg Gly			
	265	270	275
ggc aga cac cca tct gcc cat gat gtg att ctg gaa ggt gct ggt cta			919
Gly Arg His Pro Ser Ala His Asp Val Ile Leu Glu Gly Ala Gly Leu			
	280	285	290
cgg atc aca gct ccc ttg atg cca ctt ggc aag aca ctg cct tgt ggg			967
Arg Ile Thr Ala Pro Leu Met Pro Leu Gly Lys Thr Leu Pro Cys Gly			
	295	300	310
ctc acc aag act tac aca ttc agg tta aat gag cat cca agc aat aat			1015
Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn Glu His Pro Ser Asn Asn			
	315	320	325
tgg agc ccc cag ctg agt tac ttt gag tat cga agg tta ctg cgg aat			1063
Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr Arg Arg Leu Leu Arg Asn			
	330	335	340
ctc aca gcc ctc cgc atc cga gct aca tat gga gaa tac agt act ggg			1111
Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr Gly Glu Tyr Ser Thr Gly			
	345	350	355
tac att gac aat gtg acc ctg att tca gcc cgc cct gtc tct gga gcc			1159
Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala Arg Pro Val Ser Gly Ala			
	360	365	370

cca gca ccc tgg gtt gaa cag tgt ata tgt cct gtt ggg tac aag ggg	1207
Pro Ala Pro Trp Val Glu Gln Cys Ile Cys Pro Val Gly Tyr Lys Gly	
375 380 385 390	
caa ttc tgc cag gat tgt gct tct ggc tac aag aga gat tca gcg aga	1255
Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala Arg	
395 400 405	
ctg ggg cct ttt ggc acc tgt att cct tgt aac tgt caa ggg gga ggg	1303
Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly Gly	
410 415 420	
gcc tgt gat cca gac aca gga gat tgt tat tca ggg gat gag aat cct	1351
Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn Pro	
425 430 435	
gac att gag tgt gct gac tgc cca att ggt ttc tac aac gat ccg cac	1399
Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro His	
440 445 450	
gac ccc cgc agc tgc aag cca tgt ccc tgt cat aac ggg ttc agc tgc	1447
Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser Cys	
455 460 465 470	
tca gtg atg ccg gag acg gag gag gtg gtg tgc aat aac tgc cct ccc	1495
Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro Pro	
475 480 485	
ggg gtc acc ggt gcc cgc tgt gag ctc tgt gct gat ggc tac ttt ggg	1543
Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly	
490 495 500	
gac ccc ttt ggt gaa cat ggc cca gtg agg cct tgt cag ccc tgt caa	1591
Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys Gln	
505 510 515	
tgc aac aac aat gtg gac ccc agt gcc tct ggg aat tgt gac cgg ctg	1639
Cys Asn Asn Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg Leu	
520 525 530	
aca ggc agg tgt ttg aag tgt atc cac aac aca gcc ggc atc tac tgc	1687
Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr Cys	
535 540 545 550	
gac cag tgc aaa gca ggc tac ttc ggg gac cca ttg gct ccc aac cca	1735
Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn Pro	
555 560 565	
gca gac aag tgt cga gct tgc aac tgt aac ccc atg ggc tca gag cct	1783
Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu Pro	
570 575 580	
gta gga tgt cga agt gat ggc acc tgt gtt tgc aag cca gga ttt ggt	1831
Val Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe Gly	
585 590 595	
ggc ccc aac tgt gag cat gga gca ttc agc tgt cca gct tgc tat aat	1879
Gly Pro Asn Cys Glu His Gly Ala Phe Ser Cys Pro Ala Cys Tyr Asn	
600 605 610	

caa gtg aag att cag atg gat cag ttt atg cag cag ctt cag aga atg	1927
Gln Val Lys Ile Gln Met Asp Gln Phe Met Gln Gln Leu Gln Arg Met	
615 620 625 630	
gag gcc ctg att tca aag gct cag ggt ggt gat gga gta gta cct gat	1975
Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly Asp Gly Val Val Pro Asp	
635 640 645	
aca gag ctg gaa ggc agg atg cag cag gct gag cag gcc ctt cag gac	2023
Thr Glu Leu Glu Gly Arg Met Gln Gln Ala Glu Gln Ala Leu Gln Asp	
650 655 660	
att ctg aga gat gcc cag att tca gaa ggt gct agc aga tcc ctt ggt	2071
Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly Ala Ser Arg Ser Leu Gly	
665 670 675	
ctc cag ttg gcc aag gtg agg agc caa gag aac agc tac cag agc cgc	2119
Leu Gln Leu Ala Lys Val Arg Ser Gln Glu Asn Ser Tyr Gln Ser Arg	
680 685 690	
ctg gat gac ctc aag atg act gtg gaa aga gtt cgg gct ctg gga agt	2167
Leu Asp Asp Leu Lys Met Thr Val Glu Arg Val Arg Ala Leu Gly Ser	
695 700 705 710	
cag tac cag aac cga gtt cgg gat act cac agg ctc atc act cag atg	2215
Gln Tyr Gln Asn Arg Val Arg Asp Thr His Arg Leu Ile Thr Gln Met	
715 720 725	
cag ctg agc ctg gca gaa agt gaa gct tcc ttg gga aac act aac att	2263
Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser Leu Gly Asn Thr Asn Ile	
730 735 740	
cct gcc tca gac cac tac gtg ggg cca aat ggc ttt aaa agt ctg gct	2311
Pro Ala Ser Asp His Tyr Val Gly Pro Asn Gly Phe Lys Ser Leu Ala	
745 750 755	
cag gag gcc aca aga tta gca gaa agc cac gtt gag tca gcc agt aac	2359
Gln Glu Ala Thr Arg Leu Ala Glu Ser His Val Glu Ser Ala Ser Asn	
760 765 770	
atg gag caa ctg aca agg gaa act gag gac tat tcc aaa caa gcc ctc	2407
Met Glu Gln Leu Thr Arg Glu Thr Glu Asp Tyr Ser Lys Gln Ala Leu	
775 780 785 790	
tca ctg gtg cgc aag gcc ctg cat gaa gga gtc gga agc gga agc ggt	2455
Ser Leu Val Arg Lys Ala Leu His Glu Gly Val Gly Ser Gly Ser Gly	
795 800 805	
agc ccg gac ggt gct gtg gtg caa ggg ctt gtg gaa aaa ttg gag aaa	2503
Ser Pro Asp Gly Ala Val Val Gln Gly Leu Val Glu Lys Leu Glu Lys	
810 815 820	
acc aag tcc ctg gcc cag cag ttg aca agg gag gcc act caa gcg gaa	2551
Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg Glu Ala Thr Gln Ala Glu	
825 830 835	
att gaa gca gat agg tct tat cag cac agt ctc cgc ctc ctg gat tca	2599
Ile Glu Ala Asp Arg Ser Tyr Gln His Ser Leu Arg Leu Leu Asp Ser	
840 845 850	
gtg tct ccg ctt cag gga gtc agt gat cag tcc ttt cag gtg gaa gaa	2647

Val 855	Ser	Pro	Leu	Gln	Gly 860	Val	Ser	Asp	Gln	Ser 865	Phe	Gln	Val	Glu	Glu 870		
gca	aag	agg	atc	aaa	caa	aaa	gcg	gat	tca	ctc	tca	agc	ctg	gta	acc	2695	
Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser	Leu	Ser	Ser	Leu	Val	Thr	885	
				875					880								
agg	cat	atg	gat	gag	ttc	aag	cgt	aca	caa	aag	aat	ctg	gga	aac	tgg	2743	
Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln	Lys	Asn	Leu	Gly	Asn	Trp	900	
			890					895					900				
aaa	gaa	gaa	gca	cag	cag	ctc	tta	cag	aat	gga	aaa	agt	ggg	aga	gag	2791	
Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn	Gly	Lys	Ser	Gly	Arg	Glu	915	
		905					910										
aaa	tca	gat	cag	ctg	ctt	tcc	cgt	gcc	aat	ctt	gct	aaa	agc	aga	gca	2839	
Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn	Leu	Ala	Lys	Ser	Arg	Ala	930	
	920					925					930						
caa	gaa	gca	ctg	agt	atg	ggc	aat	gcc	act	ttt	tat	gaa	gtt	gag	agc	2887	
Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr	Phe	Tyr	Glu	Val	Glu	Ser	950	
935					940					945							
atc	ctt	aaa	aac	ctc	aga	gag	ttt	gac	ctg	cag	gtg	gac	aac	aga	aaa	2935	
Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu	Gln	Val	Asp	Asn	Arg	Lys	965	
				955					960								
gca	gaa	gct	gaa	gaa	gcc	atg	aag	aga	ctc	tcc	tac	atc	agc	cag	aag	2983	
Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu	Ser	Tyr	Ile	Ser	Gln	Lys	980	
			970					975									
gtt	tca	gat	gcc	agt	gac	aag	acc	cag	caa	gca	gaa	aga	gcc	ctg	ggg	3031	
Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln	Ala	Glu	Arg	Ala	Leu	Gly	995	
		985				990											
agc	gct	gct	gct	gat	gca	cag	agg	gca	aag	aat	ggg	gcc	ggg	gag	gcc	3079	
Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys	Asn	Gly	Ala	Gly	Glu	Ala	1000	
						1005					1010						
ctg	gaa	atc	tcc	agt	gag	att	gaa	cag	gag	att	ggg	agt	ctg	aac	ttg	3127	
Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu	Ile	Gly	Ser	Leu	Asn	Leu	1015	
					1020					1025					1030		
gaa	gcc	aat	gtg	aca	gca	gat	gga	gcc	ttg	gcc	atg	gaa	aag	gga	ctg	3175	
Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu	Ala	Met	Glu	Lys	Gly	Leu	1035	
								1040						1045			
gcc	tct	ctg	aag	agt	gag	atg	agg	gaa	gtg	gaa	gga	gag	ctg	gaa	agg	3223	
Ala	Ser	Leu	Lys	Ser	Glu	Met	Arg	Glu	Val	Glu	Gly	Glu	Leu	Glu	Arg	1050	
								1055					1060				
aag	gag	ctg	gag	ttt	gac	acg	aat	atg	gat	gca	gta	cag	atg	gtg	att	3271	
Lys	Glu	Leu	Glu	Phe	Asp	Thr	Asn	Met	Asp	Ala	Val	Gln	Met	Val	Ile	1065	
							1070					1075					
aca	gaa	gcc	cag	aag	gtt	gat	acc	aga	gcc	aag	aac	gct	ggg	gtt	aca	3319	
Thr	Glu	Ala	Gln	Lys	Val	Asp	Thr	Arg	Ala	Lys	Asn	Ala	Gly	Val	Thr	1080	
						1085					1090						
atc	caa	gac	aca	ctc	aac	aca	tta	gac	ggc	ctc	ctg	cat	ctg	atg	gac	3367	
Ile	Gln	Asp	Thr	Leu	Asn	Thr	Leu	Asp	Gly	Leu	Leu	His	Leu	Met	Asp		



1095		1100		1105		1110	
cag cct ctc agt gta gat gaa gag ggg ctg gtc tta ctg gag cag aag	3415						
Gln Pro Leu Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln Lys							
		1115		1120		1125	
ctt tcc cga gcc aag acc cag atc aac agc caa ctg cgg ccc atg atg	3453						
Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met Met							
		1130		1135		1140	
tca gag ctg gaa gag agg gca cgt cag cag agg ggc cac ctc cat ttg	3511						
Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His Leu							
		1145		1150		1155	
ctg gag aca agc ata gat ggg att ctg gct gat gtg aag aac ttg gag	3559						
Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu Glu							
		1160		1165		1170	
aac att agg gac aac ctg ccc cca ggc tgc tac aat acc cag gct ctt	3607						
Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln Ala Leu							
		1175		1180		1185	1190
gag caa cag tgaagctgcc ataaatatatt ctcaactgag gttcttgagg							3656
Glu Gln Gln							
tacagatctc agggctcggg agccatgtca tgtgagtggg tgggatgggg acatttgaac							3716
atgt							3720

```
<210> 30
<211> 1193
<212> PRT
<213> Homo sapiens
```

```

<400> 30
Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
  1                               5                10                15

Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
      20                               25                30

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
      35                               40                45

Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
      50                               55                60

Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
      65                               70                75                80

Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
      85                               90                95

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
      100                               105                110

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
      115                               120                125

Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala

```

130	135	140
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala 145 150 155 160		
Val Thr Gly Glu Arg Cys Asp Gly Cys Arg Ser Gly Tyr Tyr Asn Leu 165 170 175		
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His 180 185 190		
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr 195 200 205		
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn 210 215 220		
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe 225 230 235 240		
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys 245 250 255		
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp 260 265 270		
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile 275 280 285		
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly 290 295 300		
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn 305 310 315 320		
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr 325 330 335		
Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr 340 345 350		
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala 355 360 365		
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys 370 375 380		
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr 385 390 395 400		
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys 405 410 415		
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr 420 425 430		
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly 435 440 445		
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys 450 455 460		

His Asn Gly Phe Ser Cys Ser Val Met Pro Glu Thr Glu Glu Val Val
465 470 475 480

Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
485 490 495

Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
500 505 510

Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn Val Asp Pro Ser Ala Ser
515 520 525

Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
530 535 540

Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545 550 555 560

Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
565 570 575

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
580 585 590

Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
595 600 605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
610 615 620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625 630 635 640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
645 650 655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
660 665 670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
675 680 685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
690 695 700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705 710 715 720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
725 730 735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
740 745 750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
755 760 765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
770 775 780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785 790 795 800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
805 810 815

Val Glu Lys Leu Gln Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
820 825 830

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
835 840 845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
850 855 860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865 870 875 880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
885 890 895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
900 905 910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
915 920 925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
930 935 940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945 950 955 960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
965 970 975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
980 985 990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
995 1000 1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu
1010 1015 1020

Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu
1025 1030 1035 1040

Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val
1045 1050 1055

Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp
1060 1065 1070

Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala
1075 1080 1085

Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly
1090 1095 1100

L u Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu

105 1110 1115 1120
 Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser
 1125 1130 1135
 Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln
 1140 1145 1150
 Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala
 1155 1160 1165
 Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys
 1170 1175 1180
 Tyr Asn Thr Gln Ala Leu Glu Gln Gln
 185 1190

<210> 31
 <211> 3620
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (3516)

<400> 31
 acc tcc agg agg gaa gtc tgt gat tgc aat ggg aag tcc agg cag tgt 48
 Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys
 1 5 10 15
 atc ttt gat cgg gaa ctt cac aga caa act ggt aat gga ttc cgc tgc 96
 Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly Asn Gly Phe Arg Cys
 20 25 30
 ctc aac tgc aat gac aac act gat ggc att cac tgc gag aag tgc aag 144
 Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His Cys Glu Lys Cys Lys
 35 40 45
 aat ggc ttt tac cgg cac aga gaa agg gac cgc tgt ttg ccc tgc aat 192
 Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg Cys Leu Pro Cys Asn
 50 55 60
 tgt aac tcc aaa ggt tct ctt agt gct cga tgt gac aac tct gga cgg 240
 Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys Asp Asn Ser Gly Arg
 65 70 75 80
 tgc agc tgt aaa cca ggt gtg aca gga gcc aga tgc gac cga tgt ctg 288
 Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg Cys Asp Arg Cys Leu
 85 90 95
 cca ggc ttc cac atg ctc acg gat gcg ggg tgc acc caa gac cag aga 336
 Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys Thr Gln Asp Gln Arg
 100 105 110
 ctg cta gac tcc aag tgt gac tgt gac cca gct ggc atc gca ggg ccc 384
 Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala Gly Ile Ala Gly Pro
 115 120 125
 tgt gac gcg ggc cgc tgt gtc tgc aag cca gct gtt act gga gaa cgc 432

Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala Val Thr Gly Glu Arg	
130 135 140	
tgt gat ggg tgt cga tca ggt tac tat aat ctg gat ggg ggg aac cct	480
Cys Asp Gly Cys Arg Ser Gly Tyr Tyr Asn Leu Asp Gly Gly Asn Pro	
145 150 155 160	
gag ggc tgt acc cag tgt ttc tgc tat ggg cat tca gcc agc tgc cgc	528
Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His Ser Ala Ser Cys Arg	
165 170 175	
agc tct gca gaa tac agt gtc cat aag atc acc tct acc ttt cat caa	576
Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr Ser Thr Phe His Gln	
180 185 190	
gat gtt gat ggc tgg aag gct gtc caa cga aat ggg tct cct gca aag	624
Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn Gly Ser Pro Ala Lys	
195 200 205	
ctc caa tgg tca cag cgc cat caa gat gtg ttt agc tca gcc caa cga	672
Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe Ser Ser Ala Gln Arg	
210 215 220	
cta gac cct gtc tat ttt gtg gct cct gcc aaa ttt ctt ggg aat caa	720
Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys Phe Leu Gly Asn Gln	
225 230 235 240	
cag gtg agc tat ggg caa agc ctg tcc ttt gac tac cgt gtg gac aga	768
Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp Tyr Arg Val Asp Arg	
245 250 255	
gga ggc aga cac cca tct gcc cat gat gtg att ctg gaa ggt gct ggt	816
Gly Gly Arg His Pro Ser Ala His Asp Val Ile Leu Glu Gly Ala Gly	
260 265 270	
cta cgg atc aca gct ccc ttg atg cca ctt ggc aag aca ctg cct tgt	864
Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly Lys Thr Leu Pro Cys	
275 280 285	
ggg ctc acc aag act tac aca ttc agg tta aat gag cat cca agc aat	912
Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn Glu His Pro Ser Asn	
290 295 300	
aat tgg agc ccc cag ctg agt tac ttt gag tat cga agg tta ctg cgg	960
Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr Arg Arg Leu Leu Arg	
305 310 315 320	
aat ctc aca gcc ctc cgc atc cga gct aca tat gga gaa tac agt act	1008
Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr Gly Glu Tyr Ser Thr	
325 330 335	
ggg tac att gac aat gtg acc ctg att tca gcc cgc cct gtc tct gga	1056
Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala Arg Pro Val Ser Gly	
340 345 350	
gcc cca gca ccc tgg gtt gaa cag tgt ata tgt cct gtt ggg tac aag	1104
Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys Pro Val Gly Tyr Lys	
355 360 365	
ggg caa ttc tgc cag gat tgt gct tct ggc tac aag aga gat tca gcg	1152
Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala	

370	375	380	
aga ctg ggg cct ttt ggc acc tgt att cct tgt aac tgt caa ggg gga			1200
Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly			
385	390	395	400
ggg gcc tgt gat cca gac aca gga gat tgt tat tca ggg gat gag aat			1248
Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn			
	405	410	415
cct gac att gag tgt gct gac tgc cca att ggt ttc tac aac gat ccg			1296
Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro			
	420	425	430
cac gac ccc cgc agc tgc aag cca tgt ccc tgt cat aac ggg ttc agc			1344
His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser			
	435	440	445
tgc tca gtg atg ccg gag acg gag gag gtg gtg tgc aat aac tgc cct			1392
Cys Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro			
	450	455	460
ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt gct gat ggc tac ttt			1440
Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe			
	465	470	480
ggg gac ccc ttt ggt gaa cat ggc cca gtg agg cct tgt cag ccc tgt			1488
Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys			
	485	490	495
caa tgc aac aac aat gtg gac ccc agt gcc tct ggg aat tgt gac cgg			1536
Gln Cys Asn Asn Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg			
	500	505	510
ctg aca ggc agg tgt ttg aag tgt atc cac aac aca gcc ggc atc tac			1584
Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr			
	515	520	525
tgc gac cag tgc aaa gca ggc tac ttc ggg gac cca ttg gct ccc aac			1632
Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn			
	530	535	540
cca gca gac aag tgt cga gct tgc aac tgt aac ccc atg ggc tca gag			1680
Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu			
	545	550	555
cct gta gga tgt cga agt gat ggc acc tgt gtt tgc aag cca gga ttt			1728
Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe			
	565	570	575
ggt ggc ccc aac tgt gag cat gga gca ttc agc tgt cca gct tgc tat			1776
Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser Cys Pro Ala Cys Tyr			
	580	585	590
aat caa gtg aag att cag atg gat cag ttt atg cag cag ctt cag aga			1824
Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met Gln Gln Leu Gln Arg			
	595	600	605
atg gag gcc ctg att tca aag gct cag ggt ggt gat gga gta gta cct			1872
Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly Asp Gly Val Val Pro			
	610	615	620

gat aca gag ctg gaa ggc agg atg cag cag gct gag cag gcc ctt cag Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala Glu Gln Ala Leu Gln 625 630 635 640	1920
gac att ctg aga gat gcc cag att tca gaa ggt gct agc aga tcc ctt Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly Ala Ser Arg Ser Leu 645 650 655	1968
ggt ctc cag ttg gcc aag gtg agg agc caa gag aac agc tac cag agc Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu Asn Ser Tyr Gln Ser 660 665 670	2016
cgc ctg gat gac ctc aag atg act gtg gaa aga gtt cgg gct ctg gga Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg Val Arg Ala Leu Gly 675 680 685	2064
agt cag tac cag aac cga gtt cgg gat act cac agg ctc atc act cag Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His Arg Leu Ile Thr Gln 690 695 700	2112
atg cag ctg agc ctg gca gaa agt gaa gct tcc ttg gga aac act aac Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser Leu Gly Asn Thr Asn 705 710 715 720	2160
att cct gcc tca gac cac tac gtg ggg cca aat ggc ttt aaa agt ctg Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn Gly Phe Lys Ser Leu 725 730 735	2208
gct cag gag gcc aca aga tta gca gaa agc cac gtt gag tca gcc agt Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His Val Glu Ser Ala Ser 740 745 750	2256
aac atg gag caa ctg aca agg gaa act gag gac tat tcc aaa caa gcc Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp Tyr Ser Lys Gln Ala 755 760 765	2304
ctc tca ctg gtg cgc aag gcc ctg cat gaa gga gtc gga agc gga agc Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly Val Gly Ser Gly Ser 770 775 780	2352
ggt agc ccg gac ggt gct gtg gtg caa ggg ctt gtg gaa aaa ttg gag Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu Val Glu Lys Leu Glu 785 790 795 800	2400
aaa acc aag tcc ctg gcc cag cag ttg aca agg gag gcc act caa gcg Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg Glu Ala Thr Gln Ala 805 810 815	2448
gaa att gaa gca gat agg tct tat cag cac agt ctc cgc ctc ctg gat Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser Leu Arg Leu Leu Asp 820 825 830	2496
tca gtg tct ccg ctt cag gga gtc agt gat cag tcc ttt cag gtg gaa Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln Ser Phe Gln Val Glu 835 840 845	2544
gaa gca aag agg atc aaa caa aaa gcg gat tca ctc tca agc ctg gta Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser Leu Ser Ser Leu Val 850 855 860	2592

acc agg cat atg gat gag ttc aag cgt aca caa aag aat ctg gga aac	2640
Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln Lys Asn Leu Gly Asn	
865 870 875 880	
tgg aaa gaa gaa gca cag cag ctc tta cag aat gga aaa agt ggg aga	2688
Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn Gly Lys Ser Gly Arg	
885 890 895	
gag aaa tca gat cag ctg ctt tcc cgt gcc aat ctt gct aaa agc aga	2736
Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn Leu Ala Lys Ser Arg	
900 905 910	
gca caa gaa gca ctg agt atg ggc aat gcc act ttt tat gaa gtt gag	2784
Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr Phe Tyr Glu Val Glu	
915 920 925	
agc atc ctt aaa aac ctc aga gag ttt gac ctg cag gtg gac aac aga	2832
Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu Gln Val Asp Asn Arg	
930 935 940	
aaa gca gaa gct gaa gaa gcc atg aag aga ctc tcc tac atc agc cag	2880
Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu Ser Tyr Ile Ser Gln	
945 950 955 960	
aag gtt tca gat gcc agt gac aag acc cag caa gca gaa aga gcc ctg	2928
Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln Ala Glu Arg Ala Leu	
965 970 975	
ggg agc gct gct gct gat gca cag agg gca aag aat ggg gcc ggg gag	2976
Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys Asn Gly Ala Gly Glu	
980 985 990	
gcc ctg gaa atc tcc agt gag att gaa cag gag att ggg agt ctg aac	3024
Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu Ile Gly Ser Leu Asn	
995 1000 1005	
ttg gaa gcc aat gtg aca gca gat gga gcc ttg gcc atg gaa aag gga	3072
Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu Ala Met Glu Lys Gly	
1010 1015 1020	
ctg gcc tct ctg aag agt gag atg agg gaa gtg gaa gga gag ctg gaa	3120
Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val Glu Gly Glu Leu Glu	
1025 1030 1035 1040	
agg aag gag ctg gag ttt gac acg aat atg gat gca gta cag atg gtg	3168
Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp Ala Val Gln Met Val	
1045 1050 1055	
att aca gaa gcc cag aag gtt gat acc aga gcc aag aac gct ggg gtt	3216
Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala Lys Asn Ala Gly Val	
1060 1065 1070	
aca atc caa gac aca ctc aac aca tta gac ggc ctc ctg cat ctg atg	3264
Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met	
1075 1080 1085	
gac cag cct ctc agt gta gat gaa gag ggg ctg gtc tta ctg gag cag	3312
Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln	
1090 1095 1100	
aag ctt tcc cga gcc aag acc cag atc aac agc caa ctg cgg ccc atg	3360

Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met
 1105 1110 1115 1120
 atg tca gag ctg gaa gag agg gca cgt cag cag agg ggc cac ctc cat 3408
 Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His
 1125 1130 1135
 ttg ctg gag aca agc ata gat ggg att ctg gct gat gtg aag aac ttg 3456
 Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu
 1140 1145 1150
 gag aac att agg gac aac ctg ccc cca ggc tgc tac aat acc cag gct 3504
 Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln Ala
 1155 1160 1165
 ctt gag caa cag tgaagctgcc ataaatatatt ctcaactgag gttcttgagg 3556
 Leu Glu Gln Gln
 1170
 tacagatctc agggctcggg agccatgtca tgtgagtggg tgggatgggg acatttgaac 3616
 atgt 3620

<210> 32
 <211> 1172
 <212> PRT
 <213> Homo sapiens

<400> 32
 Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys
 1 5 10 15
 Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly Asn Gly Phe Arg Cys
 20 25 30
 Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His Cys Glu Lys Cys Lys
 35 40 45
 Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg Cys Leu Pro Cys Asn
 50 55 60
 Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys Asp Asn Ser Gly Arg
 65 70 75 80
 Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg Cys Asp Arg Cys Leu
 85 90 95
 Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys Thr Gln Asp Gln Arg
 100 105 110
 Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala Gly Ile Ala Gly Pro
 115 120 125
 Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala Val Thr Gly Glu Arg
 130 135 140
 Cys Asp Gly Cys Arg Ser Gly Tyr Tyr Asn Leu Asp Gly Gly Asn Pro
 145 150 155 160
 Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His Ser Ala Ser Cys Arg

165 170 175

Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr Ser Thr Phe His Gln
180 185 190

Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn Gly Ser Pro Ala Lys
195 200 205

Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe Ser Ser Ala Gln Arg
210 215 220

Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys Phe Leu Gly Asn Gln
225 230 235 240

Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp Tyr Arg Val Asp Arg
245 250 255

Gly Gly Arg His Pro Ser Ala His Asp Val Ile Leu Glu Gly Ala Gly
260 265 270

Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly Lys Thr Leu Pro Cys
275 280 285

Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn Glu His Pro Ser Asn
290 295 300

Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr Arg Arg Leu Leu Arg
305 310 315 320

Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr Gly Glu Tyr Ser Thr
325 330 335

Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala Arg Pro Val Ser Gly
340 345 350

Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys Pro Val Gly Tyr Lys
355 360 365

Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala
370 375 380

Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly
385 390 395 400

Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn
405 410 415

Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro
420 425 430

His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser
435 440 445

Cys Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro
450 455 460

Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe
465 470 475 480

Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys
485 490 495

Gln Cys Asn Asn Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg
500 505 510

Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr
515 520 525

Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn
530 535 540

Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu
545 550 555 560

Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe
565 570 575

Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser Cys Pro Ala Cys Tyr
580 585 590

Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met Gln Gln Leu Gln Arg
595 600 605

Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly Asp Gly Val Val Pro
610 615 620

Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala Glu Gln Ala Leu Gln
625 630 635 640

Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly Ala Ser Arg Ser Leu
645 650 655

Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu Asn Ser Tyr Gln Ser
660 665 670

Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg Val Arg Ala Leu Gly
675 680 685

Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His Arg Leu Ile Thr Gln
690 695 700

Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser Leu Gly Asn Thr Asn
705 710 715 720

Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn Gly Phe Lys Ser Leu
725 730 735

Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His Val Glu Ser Ala Ser
740 745 750

Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp Tyr Ser Lys Gln Ala
755 760 765

Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly Val Gly Ser Gly Ser
770 775 780

Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu Val Glu Lys Leu Glu
785 790 795 800

Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg Glu Ala Thr Gln Ala
805 810 815

Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser Leu Arg Leu Leu Asp
820 825 830

Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln Ser Phe Gln Val Glu
835 840 845

Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser Leu Ser Ser Leu Val
850 855 860

Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln Lys Asn Leu Gly Asn
865 870 875 880

Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn Gly Lys Ser Gly Arg
885 890 895

Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn Leu Ala Lys Ser Arg
900 905 910

Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr Phe Tyr Glu Val Glu
915 920 925

Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu Gln Val Asp Asn Arg
930 935 940

Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu Ser Tyr Ile Ser Gln
945 950 955 960

Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln Ala Glu Arg Ala Leu
965 970 975

Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys Asn Gly Ala Gly Glu
980 985 990

Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu Ile Gly Ser Leu Asn
995 1000 1005

Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu Ala Met Glu Lys Gly
1010 1015 1020

Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val Glu Gly Glu Leu Glu
1025 1030 1035 1040

Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp Ala Val Gln Met Val
1045 1050 1055

Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala Lys Asn Ala Gly Val
1060 1065 1070

Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met
1075 1080 1085

Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln
1090 1095 1100

Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met
1105 1110 1115 1120

Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His
1125 1130 1135

Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu

1140

1145

1150

Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln Ala
 1155 1160 1165

Leu Glu Gln Gln
 1170

<210> 33

<211> 5159

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (40)..(3615)

<220>

<221> sig_peptide

<222> (40)..(102)

<400> 33

tcggcacgag ggcacccgca gcgggcaggc cgcccggcc atg cct gcg ctc tgg 54
 Met Pro Ala Leu Trp
 1 5

ctc agc tgc tgc ctc ggt gtc gcg ctc ctg ctg ccc gcc agc cag gcc 102
 Leu Ser Cys Cys Leu Gly Val Ala Leu Leu Leu Pro Ala Ser Gln Ala
 10 15 20

acc tcc agg agg gaa gtc tgt gat tgc aat ggg aag tcc agg caa tgt 150
 Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys
 25 30 35

gtc ttt gat cag gag ctc cat cga caa gca ggc agc ggg ttc cgt tgc 198
 Val Phe Asp Gln Glu Leu His Arg Gln Ala Gly Ser Gly Phe Arg Cys
 40 45 50

ctc aac tgc aat gac aat aca gcg ggg gtt cac tgc gag cgg tcg agg 246
 Leu Asn Cys Asn Asp Asn Thr Ala Gly Val His Cys Glu Arg Ser Arg
 55 60 65

gag ggg ttt tac cag cat cag agc aag agc cgc tgc cta ccc tgc aac 294
 Glu Gly Phe Tyr Gln His Gln Ser Lys Ser Arg Cys Leu Pro Cys Asn
 70 75 80 85

tgc cac tca aag ggt tcc ctc agt gct gga tgt gac aac tct gga caa 342
 Cys His Ser Lys Gly Ser Leu Ser Ala Gly Cys Asp Asn Ser Gly Gln
 90 95 100

tgc agg tgt aag cca ggt gtg aca gga caa aga tgt gac cag tgt cag 390
 Cys Arg Cys Lys Pro Gly Val Thr Gly Gln Arg Cys Asp Gln Cys Gln
 105 110 115

cca ggc ttc cat atg ctc acc gat gct gga tgc acc cga gac cag ggg 438
 Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys Thr Arg Asp Gln Gly
 120 125 130

caa cta gat tcc aag tgt gac tgt gac cca gct ggc atc tct gga ccc 486
 Gln Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala Gly Ile Ser Gly Pro

135	140	145	
tgt gat tct ggc cga	tgt gtc tgc aaa cca	gcc gtc act gga gag cgc	534
Cys Asp Ser Gly Arg	Cys Val Cys Lys Pro	Ala Val Thr Gly Glu Arg	
150	155	160 165	
tgt gat ajg tgc cga	cca cgt gac tat cat	ctg gac cgg gca aac cct	582
Cys Asp Arg Cys Arg	Pro Arg Asp Tyr His	Leu Asp Arg Ala Asn Pro	
170	175	180	
gag ggc tgt acc cag	tgt ttc tgc tat ggg	cat tca gcc agc tgc cac	630
Glu Gly Cys Thr Gln	Cys Phe Cys Tyr Gly	His Ser Ala Ser Cys His	
185	190	195	
gcc tct gcc gac ttc	agt gtc cac aaa atc	act tca act ttc agt cag	678
Ala Ser Ala Asp Phe	Ser Val His Lys Ile	Thr Ser Thr Phe Ser Gln	
200	205	210	
gat gtg gat ggt tgg	aag gcg gtt cag aga	aac ggg gca cct gca aaa	726
Asp Val Asp Gly Trp	Lys Ala Val Gln Arg	Asn Gly Ala Pro Ala Lys	
215	220	225	
ctc cac tgg tca cag	cgc cat cgg gac gtg	ttt agt tct gcc cga aga	774
Leu His Trp Ser Gln	Arg His Arg Asp Val	Phe Ser Ser Ala Arg Arg	
230	235	240 245	
tca gac ccc gtc tat	ttc gtg gcc cct gcc	aaa ttc ctc ggt aac cag	822
Ser Asp Pro Val Tyr	Phe Val Ala Pro Ala	Lys Phe Leu Gly Asn Gln	
250	255	260	
caa gtg agt tac ggg	cag agc ctg tct ttt	gac tac cgc gtg gac aga	870
Gln Val Ser Tyr Gly	Gln Ser Leu Ser Phe	Asp Tyr Arg Val Asp Arg	
265	270	275	
gga ggt aga cag ccg	tct gcc tac gat gtg	atc ctg gaa ggt gct ggt	918
Gly Gly Arg Gln Pro	Ser Ala Tyr Asp Val	Ile Leu Glu Gly Ala Gly	
280	285	290	
cta cag atc aga gct	cct ctg atg gct cca	ggc aag aca ctt cct tgt	966
Leu Gln Ile Arg Ala	Pro Leu Met Ala Pro	Gly Lys Thr Leu Pro Cys	
295	300	305	
ggg atc aca aag act	tac aca ttc aga ctg	aat gaa cat cca agc agt	1014
Gly Ile Thr Lys Thr	Tyr Thr Phe Arg Leu	Asn Glu His Pro Ser Ser	
310	315	320 325	
cac tgg agt ccc cag	ctg agt tat ttc gaa	tat cga agg tta ctg cgg	1062
His Trp Ser Pro Gln	Leu Ser Tyr Phe Glu	Tyr Arg Arg Leu Leu Arg	
330	335	340	
aac ctc aca gcc ctc	ctg atg atc cga gct	acg tac gga gaa tat agt	1110
Asn Leu Thr Ala Leu	Leu Met Ile Arg Ala	Thr Tyr Gly Glu Tyr Ser	
345	350	355	
aca ggg tac att gat	aac gtg acc ctg gtt	tca gcc cgc cct gtc ctt	1158
Thr Gly Tyr Ile Asp	Asn Val Thr Leu Val	Ser Ala Arg Pro Val Leu	
360	365	370	
gga gcc cca gcc cct	tgg gtt gaa cgt tgt	gta tgc ctg ctg ggg tac	1206
Gly Ala Pro Ala Pro	Trp Val Glu Arg Cys	Val Cys Leu Leu Gly Tyr	
375	380	385	

aag gga caa ttc tgc cag gaa tgt gct tct ggt tac aaa aga gat tcg	1254
Lys Gly Gln Phe Cys Gln Glu Cys Ala Ser Gly Tyr Lys Arg Asp Ser	
390 395 400 405	
gca aga ttg ggc gct ttt ggc gcc tgt gtt ccc tgt aac tgc caa ggg	1302
Ala Arg Leu Gly Ala Phe Gly Ala Cys Val Pro Cys Asn Cys Gln Gly	
410 415 420	
gag ggg gcc tgt gat cca gac acg gga gat tgc tac tcg ggg gac gag	1350
Glu Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu	
425 430 435	
aat cct gac att gag tgt gct gac tgt ccc atc ggt ttc tac aat gac	1398
Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp	
440 445 450	
cca cat gac ccc cgc agc tgc aag cca tgt ccc tgt cac aat ggg ttc	1446
Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe	
455 460 465	
agc tgt tca gtg atg cct gag aca gag gag gtg gtg tgt aac aac tgt	1494
Ser Cys Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys	
470 475 480 485	
ccc cct ggg gtc aca ggt gcc cgc tgt gag ctc tgt gct gat ggc ttc	1542
Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Phe	
490 495 500	
ttt ggg gat ccc ttt ggg gaa cat ggc cca gtg agg cct tgt caa cgc	1590
Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Arg	
505 510 515	
tgc caa tgc aac aac aac gtg gac ccc aat gcc tct ggg aac tgt gac	1638
Cys Gln Cys Asn Asn Asn Val Asp Pro Asn Ala Ser Gly Asn Cys Asp	
520 525 530	
cag ttg aca ggc aga tgc ttg aaa tgt atc tac aac acg gcc ggt gtc	1686
Gln Leu Thr Gly Arg Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Val	
535 540 545	
tac tgt gac cag tgc aaa gca ggt tac ttt gga gac cca ttg gct ccc	1734
Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro	
550 555 560 565	
aac cca gca gac aag tgt cga gct tgc aac tgc agc ccc atg ggt gcg	1782
Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Ser Pro Met Gly Ala	
570 575 580	
gag cct gga gag tgt cga ggt gat ggc agc tgt gtt tgc aag cca ggc	1830
Glu Pro Gly Glu Cys Arg Gly Asp Gly Ser Cys Val Cys Lys Pro Gly	
585 590 595	
ttt ggc gcc ttc aac tgt gat cac gca gcc cta acc agt tgt cct gct	1878
Phe Gly Ala Phe Asn Cys Asp His Ala Ala Leu Thr Ser Cys Pro Ala	
600 605 610	
tgc tac aat caa gtg aag att cag atg gac cag ttt acc cag cag ctc	1926
Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Thr Gln Gln Leu	
615 620 625	

cag agc ctg gag gcc ctg gtt tca aag gct cag ggt ggt ggt ggt ggt	1974
Gln Ser Leu Glu Ala Leu Val Ser Lys Ala Gln Gly Gly Gly Gly Gly	
630 635 640 645	
ggt aca gtc cca gtg cag ctg gaa ggc agg atc gag cag gct gag cag	2022
Gly Thr Val Pro Val Gln Leu Glu Gly Arg Ile Glu Gln Ala Glu Gln	
650 655 660	
gcc ctt cag gac att ctg gga gaa gct cag att tca gaa ggg gca atg	2070
Ala Leu Gln Asp Ile Leu Gly Glu Ala Gln Ile Ser Glu Gly Ala Met	
665 670 675	
aga gcc gtt gct gtc cgg ctg gcc aag gca agg agc caa gag aac gac	2118
Arg Ala Val Ala Val Arg Leu Ala Lys Ala Arg Ser Gln Glu Asn Asp	
680 685 690	
tac aag acc cgc ctg gat gac ctc aag atg act gca gaa agg atc cgg	2166
Tyr Lys Thr Arg Leu Asp Asp Leu Lys Met Thr Ala Glu Arg Ile Arg	
695 700 705	
gcc ctg ggc agt cag cat cag aac aga gtt cag gat acg agc aga ctc	2214
Ala Leu Gly Ser Gln His Gln Asn Arg Val Gln Asp Thr Ser Arg Leu	
710 715 720 725	
atc tct cag atg cgc ctg agt ctg gca gga agc gaa gct ctc ttg gaa	2262
Ile Ser Gln Met Arg Leu Ser Leu Ala Gly Ser Glu Ala Leu Leu Glu	
730 735 740	
aac act aat atc cat tct tct gag cac tac gtg ggg ccg aat gat ttt	2310
Asn Thr Asn Ile His Ser Ser Glu His Tyr Val Gly Pro Asn Asp Phe	
745 750 755	
aaa agt ctg gct cag gag gct aca aga aag gca gac agc cac gct gag	2358
Lys Ser Leu Ala Gln Glu Ala Thr Arg Lys Ala Asp Ser His Ala Glu	
760 765 770	
tca gct aac gca atg aag caa cta gca agg gaa act gag gac tac tcc	2406
Ser Ala Asn Ala Met Lys Gln Leu Ala Arg Glu Thr Glu Asp Tyr Ser	
775 780 785	
aaa caa gca ctt tca ttg gcc cgc aag ctc ttg agt gga gga ggc gga	2454
Lys Gln Ala Leu Ser Leu Ala Arg Lys Leu Leu Ser Gly Gly Gly Gly	
790 795 800 805	
agt ggc tct tgg gac agc tcc gtg gta caa ggt ctt atg gga aaa tta	2502
Ser Gly Ser Trp Asp Ser Ser Val Val Gln Gly Leu Met Gly Lys Leu	
810 815 820	
gag aaa acc aag tcc ctg agc cag cag ctg tca ttg gag ggc acc caa	2550
Glu Lys Thr Lys Ser Leu Ser Gln Gln Leu Ser Leu Glu Gly Thr Gln	
825 830 835	
gcc gac att gaa gct gat agg tcg tat cag cac agt ctc cgc ctc ctg	2598
Ala Asp Ile Glu Ala Asp Arg Ser Tyr Gln His Ser Leu Arg Leu Leu	
840 845 850	
gat tct gcc tct cag ctt cag gga gtc agt gat ctg tcc ttt cag gtg	2646
Asp Ser Ala Ser Gln Leu Gln Gly Val Ser Asp Leu Ser Phe Gln Val	
855 860 865	
gaa gca aag agg atc aga caa aag gct gat tct ctc tca aac ctg gtg	2694

Glu Ala Lys Arg Ile Arg Gln Lys Ala Asp Ser Leu Ser Asn Leu Val	
870 875 880 885	
acc aga caa acg gat gca ttc acg cgt gtg cga aac aat ctg ggg aac	2742
Thr Arg Gln Thr Asp Ala Phe Thr Arg Val Arg Asn Asn Leu Gly Asn	
890 895 900	
tgg gaa aaa gaa aca cgg cag ctt tta cag act gga aag gat agg aga	2790
Trp Glu Lys Glu Thr Arg Gln Leu Leu Gln Thr Gly Lys Asp Arg Arg	
905 910 915	
cag act tca gat cag ctg ctt tcc cgt gcc aac ctt gct aaa aac aga	2838
Gln Thr Ser Asp Gln Leu Leu Ser Arg Ala Asn Leu Ala Lys Asn Arg	
920 925 930	
gcc caa gaa gcg cta agt atg ggc aat gcc act ttt tat gaa gtt gag	2886
Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr Phe Tyr Glu Val Glu	
935 940 945	
aac atc ctg aag aac ctc cga gag ttt gat ctg cag gtt gaa gac aga	2934
Asn Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu Gln Val Glu Asp Arg	
950 955 960 965	
aaa gca gag gct gaa gag gcc atg aag aga ctc tcc tct att agc cag	2982
Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu Ser Ser Ile Ser Gln	
970 975 980	
aag gtt gcg gat gcc agt gac aag acc cag caa gca gaa acg gcc ctg	3030
Lys Val Ala Asp Ala Ser Asp Lys Thr Gln Gln Ala Glu Thr Ala Leu	
985 990 995	
ggg agc gcc act gcc gac acc caa cgg gca aag aac gca gct agg gag	3078
Gly Ser Ala Thr Ala Asp Thr Gln Arg Ala Lys Asn Ala Ala Arg Glu	
1000 1005 1010	
gcc ctg gag atc agc agc gag ata gag ctg gag ata ggg agt ctg aac	3126
Ala Leu Glu Ile Ser Ser Glu Ile Glu Leu Glu Ile Gly Ser Leu Asn	
1015 1020 1025	
ttg gaa gct aat gtg aca gca gat ggg gcc ttg gcc atg gag aaa ggg	3174
Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu Ala Met Glu Lys Gly	
1030 1035 1040 1045	
act gcc act ctg aag agc gag atg aga gag atg att gag ctg gcc aga	3222
Thr Ala Thr Leu Lys Ser Glu Met Arg Glu Met Ile Glu Leu Ala Arg	
1050 1055 1060	
aag gag ctg gag ttt gac acg gat aag gac acg gtg cag ctg gtg att	3270
Lys Glu Leu Glu Phe Asp Thr Asp Lys Asp Thr Val Gln Leu Val Ile	
1065 1070 1075	
act gaa gcc cag caa gct gat gcc aga gcc acg agt gcc gga gtt acc	3318
Thr Glu Ala Gln Gln Ala Asp Ala Arg Ala Thr Ser Ala Gly Val Thr	
1080 1085 1090	
atc caa gac acr ctc aac aca ttg gac ggc atc cta cac ctc ata gac	3366
Ile Gln Asp Xaa Leu Asn Thr Leu Asp Gly Ile Leu His Leu Ile Asp	
1095 1100 1105	
cag cct ggc agt gtg gat gaa gaa ggg atg atg cta tta gaa caa ggg	3414
Gln Pro Gly Ser Val Asp Glu Glu Gly Met Met Leu Leu Glu Gln Gly	

1110 1115 1120 1125
ctt ttc caa gcc aag acc cag atc aac agt cga ctt cgg ccc ttg atg 3462
Leu Phe Gln Ala Lys Thr Gln Ile Asn Ser Arg Leu Arg Pro Leu Met
1130 1135 1140
tct gac ctg gag gag agg gtg cgt cgg cag agg aac cac ctc cat ctg 3510
Ser Asp Leu Glu Glu Arg Val Arg Arg Gln Arg Asn His Leu His Leu
1145 1150 1155
ctg gag act agc ata gat gga att ctt gct gat gtg aag aac ctg gag 3558
Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu Glu
1160 1165 1170
aac att cga gac aac ctg ccc cca ggc tgc tac aat acc caa gct ctt 3606
Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln Ala Leu
1175 1180 1185
gag caa cag tgaagttgtc atagagattt gtccactgtt gtgaaaggac 3655
Glu Gln Gln
1190
acagacctca ggggtcagga gccatctcgt gtggatgggc tgtgctcagg ctatctgaac 3715
acatttaatg ggtttgttca ggtccaattc catccctgag accatgggct gtggatgtct 3775
tcctgtacca atataatact gtttgtactt cctgatgctg gcagtgaggc agatagcatt 3835
gagtatgaga ttgatcaagg agggacaaat cgtgcgctca gaacagtgac aaactgaatt 3895
ctgggcagtg aggcagatag cattgagtat gagattgatc aaggacctgg accccaaaga 3955
tagactggat ggaaagacaa actgcacagg cagatgtttg cctcataata gtcgtaagtg 4015
gagtcctgga atttggtcag aacagtgaaa aactggaatt ctgggatata gaaagatcct 4075
gctgctatgt caggacaaag tgagatctaa tcccgtgcg gccagcaaag tactcttgct 4135
tcaccacta gacgtttttt gtccaccaca tttcctccag tgcccacca atacatgagt 4195
atgtcctcca ctcatgctg agtgcagaga gcagtgatgg tatagatctg gaaatctggc 4255
ccatgtggag cagtgggtgcc cgctgcacc cctaaccttc atgctctcgg cctgagtgtg 4315
acagcctttc tcctaattgg gcgaacaact tagaggctgt atttttttat gaaagcatct 4375
tttaccagcc aagcaatcat tgggaaagta tttctttgag tttcaaagtg atataagaaa 4435
tgtgtctggc actaaaggaa gtggagttat ctaaaagata tattcatcat aatccaatct 4495
tcctttggaa aactaaaac tcatatacat ctgtgtattg tatcttattt tctctttctc 4555
ctctctcttt cctccacca taataagaga atgttctac tcacacttca gctgggtcac 4615
atccatccct ccattcatcc ttccatccat ctttccatcc attacctcca tccagccttc 4675
taacatatat ttattgcgtc actactgtgt gccaggggtg agtggaacag tatggacagt 4735
ctctactctc atggagttga gtgtctagt agagaacaac attagaataa gtaaattggaa 4795
actcccatgc cttgttcac tcatgtgata ttattgcag tcaccaccc tttggtttga 4855

aacctctttt cttaataatg tgttgcaaga cattcccatg agggacttg agttagagca 4915
 aagttgagat cgctctgagt tgtacacatt tctctatggt ccagccgtct ctccaccct 4975
 tccacacaga ctgtgcacag actggtgcat cagggcaata ccagtgggaa ttgctgaagg 5035
 aaccagaggc attgggacct cagtttggaa gactactgta ctgtctcacc tctgtacttc 5095
 cttgtctttt catggatgtg ttattaaata aagaacgagt gttagatgct aaaaaaaaaa 5155
 aaaa 5159

<210> 34
 <211> 1192
 <212> PRT
 <213> Mus musculus

<400> 34

Met	Pro	Ala	Leu	Trp	Leu	Ser	Cys	Cys	Leu	Gly	Val	Ala	Leu	Leu	Leu	1	5	10	15
Pro	Ala	Ser	Gln	Ala	Thr	Ser	Arg	Arg	Glu	Val	Cys	Asp	Cys	Asn	Gly	20	25	30	
Lys	Ser	Arg	Gln	Cys	Val	Phe	Asp	Gln	Glu	Leu	His	Arg	Gln	Ala	Gly	35	40	45	
Ser	Gly	Phe	Arg	Cys	Leu	Asn	Cys	Asn	Asp	Asn	Thr	Ala	Gly	Val	His	50	55	60	
Cys	Glu	Arg	Ser	Arg	Glu	Gly	Phe	Tyr	Gln	His	Gln	Ser	Lys	Ser	Arg	65	70	75	80
Cys	Leu	Pro	Cys	Asn	Cys	His	Ser	Lys	Gly	Ser	Leu	Ser	Ala	Gly	Cys	85	90	95	
Asp	Asn	Ser	Gly	Gln	Cys	Arg	Cys	Lys	Pro	Gly	Val	Thr	Gly	Gln	Arg	100	105	110	
Cys	Asp	Gln	Cys	Gln	Pro	Gly	Phe	His	Met	Leu	Thr	Asp	Ala	Gly	Cys	115	120	125	
Thr	Arg	Asp	Gln	Gly	Gln	Leu	Asp	Ser	Lys	Cys	Asp	Cys	Asp	Pro	Ala	130	135	140	
Gly	Ile	Ser	Gly	Pro	Cys	Asp	Ser	Gly	Arg	Cys	Val	Cys	Lys	Pro	Ala	145	150	155	160
Val	Thr	Gly	Glu	Arg	Cys	Asp	Arg	Cys	Arg	Pro	Arg	Asp	Tyr	His	Leu	165	170	175	
Asp	Arg	Ala	Asn	Pro	Glu	Gly	Cys	Thr	Gln	Cys	Phe	Cys	Tyr	Gly	His	180	185	190	
Ser	Ala	Ser	Cys	His	Ala	Ser	Ala	Asp	Phe	Ser	Val	His	Lys	Ile	Thr	195	200	205	
Ser	Thr	Phe	Ser	Gln	Asp	Val	Asp	Gly	Trp	Lys	Ala	Val	Gln	Arg	Asn	210	215	220	

Gly Ala Pro Ala Lys Leu His Trp Ser Gln Arg His Arg Asp Val Phe
225 230 235 240

Ser Ser Ala Arg Arg Ser Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
245 250 255

Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
260 265 270

Tyr Arg Val Asp Arg Gly Gly Arg Gln Pro Ser Ala Tyr Asp Val Ile
275 280 285

Leu Glu Gly Ala Gly Leu Gln Ile Arg Ala Pro Leu Met Ala Pro Gly
290 295 300

Lys Thr Leu Pro Cys Gly Ile Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305 310 315 320

Glu His Pro Ser Ser His Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
325 330 335

Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Leu Met Ile Arg Ala Thr
340 345 350

Tyr Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Val Ser
355 360 365

Ala Arg Pro Val Leu Gly Ala Pro Ala Pro Trp Val Glu Arg Cys Val
370 375 380

Cys Leu Leu Gly Tyr Lys Gly Gln Phe Cys Gln Glu Cys Ala Ser Gly
385 390 395 400

Tyr Lys Arg Asp Ser Ala Arg Leu Gly Ala Phe Gly Ala Cys Val Pro
405 410 415

Cys Asn Cys Gln Gly Glu Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys
420 425 430

Tyr Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile
435 440 445

Gly Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro
450 455 460

Cys His Asn Gly Phe Ser Cys Ser Val Met Pro Glu Thr Glu Glu Val
465 470 475 480

Val Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu
485 490 495

Cys Ala Asp Gly Phe Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val
500 505 510

Arg Pro Cys Gln Arg Cys Gln Cys Asn Asn Asn Val Asp Pro Asn Ala
515 520 525

Ser Gly Asn Cys Asp Gln Leu Thr Gly Arg Cys Leu Lys Cys Ile Tyr
530 535 540

Asn Thr Ala Gly Val Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly
545 550 555 560

Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys
565 570 575

Ser Pro Met Gly Ala Glu Pro Gly Glu Cys Arg Gly Asp Gly Ser Cys
580 585 590

Val Cys Lys Pro Gly Phe Gly Ala Phe Asn Cys Asp His Ala Ala Leu
595 600 605

Thr Ser Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln
610 615 620

Phe Thr Gln Gln Leu Gln Ser Leu Glu Ala Leu Val Ser Lys Ala Gln
625 630 635 640

Gly Gly Gly Gly Gly Gly Thr Val Pro Val Gln Leu Glu Gly Arg Ile
645 650 655

Glu Gln Ala Glu Gln Ala Leu Gln Asp Ile Leu Gly Glu Ala Gln Ile
660 665 670

Ser Glu Gly Ala Met Arg Ala Val Ala Val Arg Leu Ala Lys Ala Arg
675 680 685

Ser Gln Glu Asn Asp Tyr Lys Thr Arg Leu Asp Asp Leu Lys Met Thr
690 695 700

Ala Glu Arg Ile Arg Ala Leu Gly Ser Gln His Gln Asn Arg Val Gln
705 710 715 720

Asp Thr Ser Arg Leu Ile Ser Gln Met Arg Leu Ser Leu Ala Gly Ser
725 730 735

Glu Ala Leu Leu Glu Asn Thr Asn Ile His Ser Ser Glu His Tyr Val
740 745 750

Gly Pro Asn Asp Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Lys Ala
755 760 765

Asp Ser His Ala Glu Ser Ala Asn Ala Met Lys Gln Leu Ala Arg Glu
770 775 780

Thr Glu Asp Tyr Ser Lys Gln Ala Leu Ser Leu Ala Arg Lys Leu Leu
785 790 795 800

Ser Gly Gly Gly Gly Ser Gly Ser Trp Asp Ser Ser Val Val Gln Gly
805 810 815

Leu Met Gly Lys Leu Glu Lys Thr Lys Ser Leu Ser Gln Gln Leu Ser
820 825 830

Leu Glu Gly Thr Gln Ala Asp Ile Glu Ala Asp Arg Ser Tyr Gln His
835 840 845

Ser Leu Arg Leu Leu Asp Ser Ala Ser Gln Leu Gln Gly Val Ser Asp
850 855 860

Leu Ser Phe Gln Val Glu Ala Lys Arg Ile Arg Gln Lys Ala Asp Ser

865	870										875				880		
Leu Ser Asn Leu Val Thr Arg Gln Thr Asp Ala Phe Thr Arg Val Arg																	
	885										890				895		
Asn Asn Leu Gly Asn Trp Glu Lys Glu Thr Arg Gln Leu Leu Gln Thr																	
	900										905				910		
Gly Lys Asp Arg Arg Gln Thr Ser Asp Gln Leu Leu Ser Arg Ala Asn																	
	915										920				925		
Leu Ala Lys Asn Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr																	
	930										935				940		
Phe Tyr Glu Val Glu Asn Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu																	
945	950										955				960		
Gln Val Glu Asp Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu																	
	965										970				975		
Ser Ser Ile Ser Gln Lys Val Ala Asp Ala Ser Asp Lys Thr Gln Gln																	
	980										985				990		
Ala Glu Thr Ala Leu Gly Ser Ala Thr Ala Asp Thr Gln Arg Ala Lys																	
	995										1000				1005		
Asn Ala Ala Arg Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Leu Glu																	
1010	1015										1020						
Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu																	
025	1030										1035				1040		
Ala Met Glu Lys Gly Thr Ala Thr Leu Lys Ser Glu Met Arg Glu Met																	
	1045										1050				1055		
Ile Glu Leu Ala Arg Lys Glu Leu Glu Phe Asp Thr Asp Lys Asp Thr																	
	1060										1065				1070		
Val Gln Leu Val Ile Thr Glu Ala Gln Gln Ala Asp Ala Arg Ala Thr																	
	1075										1080				1085		
Ser Ala Gly Val Thr Ile Gln Asp Xaa Leu Asn Thr Leu Asp Gly Ile																	
1090	1095										1100						
Leu His Leu Ile Asp Gln Pro Gly Ser Val Asp Glu Glu Gly Met Met																	
105	1110										1115				1120		
Leu Leu Glu Gln Gly Leu Phe Gln Ala Lys Thr Gln Ile Asn Ser Arg																	
	1125										1130				1135		
Leu Arg Pro Leu Met Ser Asp Leu Glu Glu Arg Val Arg Arg Gln Arg																	
	1140										1145				1150		
Asn His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp																	
	1155										1160				1165		
Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr																	
1170	1175										1180						
Asn Thr Gln Ala Leu Glu Gln Gln																	
185	1190																

<210> 35
 <211> 5057
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1) .. (3513)

<400> 35

```

acc tcc agg agg gaa gtc tgt gat tgc aat ggg aag tcc agg caa tgt   48
Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys
   1                   5                   10                   15

gtc ttt gat cag gag ctc cat cga caa gca ggc agc ggg ttc cgt tgc   96
Val Phe Asp Gln Glu Leu His Arg Gln Ala Gly Ser Gly Phe Arg Cys
                   20                   25                   30

ctc aac tgc aat gac aat aca gcg ggg gtt cac tgc gag cgg tcg agg   144
Leu Asn Cys Asn Asp Asn Thr Ala Gly Val His Cys Glu Arg Ser Arg
                   35                   40                   45

gag ggg ttt tac cag cat cag agc aag agc cgc tgc cta ccc tgc aac   192
Glu Gly Phe Tyr Gln His Gln Ser Lys Ser Arg Cys Leu Pro Cys Asn
                   50                   55                   60

tgc cac tca aag ggt tcc ctc agt gct gga tgt gac aac tct gga caa   240
Cys His Ser Lys Gly Ser Leu Ser Ala Gly Cys Asp Asn Ser Gly Gln
                   65                   70                   75                   80

tgc agg tgt aag cca ggt gtg aca gga caa aga tgt gac cag tgt cag   288
Cys Arg Cys Lys Pro Gly Val Thr Gly Gln Arg Cys Asp Gln Cys Gln
                   85                   90                   95

cca ggc ttc cat atg ctc acc gat gct gga tgc acc cga gac cag ggg   336
Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys Thr Arg Asp Gln Gly
                   100                  105                  110

caa cta gat tcc aag tgt gac tgt gac cca gct ggc atc tct gga ccc   384
Gln Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala Gly Ile Ser Gly Pro
                   115                  120                  125

tgt gat tct ggc cga tgt gtc tgc aaa cca gcc gtc act gga gag cgc   432
Cys Asp Ser Gly Arg Cys Val Cys Lys Pro Ala Val Thr Gly Glu Arg
                   130                  135                  140

tgt gat agg tgc cga cca cgt gac tat cat ctg gac cgg gca aac cct   480
Cys Asp Arg Cys Arg Pro Arg Asp Tyr His Leu Asp Arg Ala Asn Pro
                   145                  150                  155                  160

gag ggc tgt acc cag tgt ttc tgc tat ggg cat tca gcc agc tgc cac   528
Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His Ser Ala Ser Cys His
                   165                  170                  175

gcc tct gcc gac ttc agt gtc cac aaa atc act tca act ttc agt cag   576
Ala Ser Ala Asp Phe Ser Val His Lys Ile Thr Ser Thr Phe Ser Gln
                   180                  185                  190

gat gtg gat ggt tgg aag gcg gtt cag aga aac ggg gca cct gca aaa   624

```

Asp	Val	Asp	Gly	Trp	Lys	Ala	Val	Gln	Arg	Asn	Gly	Ala	Pro	Ala	Lys	
	195						200					205				
ctc	cac	tgg	tca	cag	cgc	cat	cgg	gac	gtg	ttt	agt	tct	gcc	cga	aga	672
Leu	His	Trp	Ser	Gln	Arg	His	Arg	Asp	Val	Phe	Ser	Ser	Ala	Arg	Arg	
	210					215					220					
tca	gac	ccc	gtc	tat	ttc	gtg	gcc	cct	gcc	aaa	ttc	ctc	ggt	aac	cag	720
Ser	Asp	Pro	Val	Tyr	Phe	Val	Ala	Pro	Ala	Lys	Phe	Leu	Gly	Asn	Gln	
225					230					235					240	
caa	gtg	agt	tac	ggg	cag	agc	ctg	tct	ttt	gac	tac	cgc	gtg	gac	aga	768
Gln	Val	Ser	Tyr	Gly	Gln	Ser	Leu	Ser	Phe	Asp	Tyr	Arg	Val	Asp	Arg	
				245					250					255		
gga	ggt	aga	cag	ccg	tct	gcc	tac	gat	gtg	atc	ctg	gaa	ggt	gct	ggt	816
Gly	Gly	Arg	Gln	Pro	Ser	Ala	Tyr	Asp	Val	Ile	Leu	Glu	Gly	Ala	Gly	
			260					265					270			
cta	cag	atc	aga	gct	cct	ctg	atg	gct	cca	ggc	aag	aca	ctt	cct	tgt	864
Leu	Gln	Ile	Arg	Ala	Pro	Leu	Met	Ala	Pro	Gly	Lys	Thr	Leu	Pro	Cys	
	275					280						285				
ggg	atc	aca	aag	act	tac	aca	ttc	aga	ctg	aat	gaa	cat	cca	agc	agt	912
Gly	Ile	Thr	Lys	Thr	Tyr	Thr	Phe	Arg	Leu	Asn	Glu	His	Pro	Ser	Ser	
	290					295					300					
cac	tgg	agt	ccc	cag	ctg	agt	tat	ttc	gaa	tat	cga	agg	tta	ctg	cgg	960
His	Trp	Ser	Pro	Gln	Leu	Ser	Tyr	Phe	Glu	Tyr	Arg	Arg	Leu	Leu	Arg	
305				310					315						320	
aac	ctc	aca	gcc	ctc	ctg	atg	atc	cga	gct	acg	tac	gga	gaa	tat	agt	1008
Asn	Leu	Thr	Ala	Leu	Leu	Met	Ile	Arg	Ala	Thr	Tyr	Gly	Glu	Tyr	Ser	
				325				330						335		
aca	ggg	tac	att	gat	aac	gtg	acc	ctg	gtt	tca	gcc	cgc	cct	gtc	ctt	1056
Thr	Gly	Tyr	Ile	Asp	Asn	Val	Thr	Leu	Val	Ser	Ala	Arg	Pro	Val	Leu	
			340					345					350			
gga	gcc	cca	gcc	cct	tgg	gtt	gaa	cgt	tgt	gta	tgc	ctg	ctg	ggg	tac	1104
Gly	Ala	Pro	Ala	Pro	Trp	Val	Glu	Arg	Cys	Val	Cys	Leu	Leu	Gly	Tyr	
	355					360						365				
aag	gga	caa	ttc	tgc	cag	gaa	tgt	gct	tct	ggt	tac	aaa	aga	gat	tcg	1152
Lys	Gly	Gln	Phe	Cys	Gln	Glu	Cys	Ala	Ser	Gly	Tyr	Lys	Arg	Asp	Ser	
	370					375					380					
gca	aga	ttg	ggc	gct	ttt	ggc	gcc	tgt	gtt	ccc	tgt	aac	tgc	caa	ggg	1200
Ala	Arg	Leu	Gly	Ala	Phe	Gly	Ala	Cys	Val	Pro	Cys	Asn	Cys	Gln	Gly	
385					390					395					400	
gag	ggg	gcc	tgt	gat	cca	gac	acg	gga	gat	tgc	tac	tcg	ggg	gac	gag	1248
Glu	Gly	Ala	Cys	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Tyr	Ser	Gly	Asp	Glu	
				405				410						415		
aat	cct	gac	att	gag	tgt	gct	gac	tgt	ccc	atc	ggt	ttc	tac	aat	gac	1296
Asn	Pro	Asp	Il	Glu	Cys	Ala	Asp	Cys	Pro	Ile	Gly	Phe	Tyr	Asn	Asp	
			420					425					430			
cca	cat	gac	ccc	cgc	agc	tgc	aag	cca	tgt	ccc	tgt	cac	aat	ggg	ttc	1344
Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys	His	Asn	Gly	Phe	

435	440	445	
agc tgt tca gtg atg cct gag aca gag gag gtg gtg tgt aac aac tgt			1392
Ser Cys Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys			
450	455	460	
ccc cct ggg gtc aca ggt gcc cgc tgt gag ctc tgt gct gat ggc ttc			1440
Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Phe			
465	470	475	480
ttt ggg gat ccc ttt ggg gaa cat ggc cca gtg agg cct tgt caa cgc			1488
Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Arg			
	485	490	495
tgc caa tgc aac aac aac gtg gac ccc aat gcc tct ggg aac tgt gac			1536
Cys Gln Cys Asn Asn Asn Val Asp Pro Asn Ala Ser Gly Asn Cys Asp			
	500	505	510
cag ttg aca ggc aga tgc ttg aaa tgt atc tac aac acg gcc ggt gtc			1584
Gln Leu Thr Gly Arg Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Val			
	515	520	525
tac tgt gac cag tgc aaa gca ggt tac ttt gga gac cca ttg gct ccc			1632
Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro			
	530	535	540
aac cca gca gac aag tgt cga gct tgc aac tgc agc ccc atg ggt gcg			1680
Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Ser Pro Met Gly Ala			
	545	550	555
gag cct gga gag tgt cga ggt gat ggc agc tgt gtt tgc aag cca ggc			1728
Glu Pro Gly Glu Cys Arg Gly Asp Gly Ser Cys Val Cys Lys Pro Gly			
	565	570	575
ttt ggc gcc ttc aac tgt gat cac gca gcc cta acc agt tgt cct gct			1776
Phe Gly Ala Phe Asn Cys Asp His Ala Ala Leu Thr Ser Cys Pro Ala			
	580	585	590
tgc tac aat caa gtg aag att cag atg gac cag ttt acc cag cag ctc			1824
Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Thr Gln Gln Leu			
	595	600	605
cag agc ctg gag gcc ctg gtt tca aag gct cag ggt ggt ggt ggt			1872
Gln Ser Leu Glu Ala Leu Val Ser Lys Ala Gln Gly Gly Gly Gly Gly			
	610	615	620
ggt aca gtc cca gtg cag ctg gaa ggc agg atc gag cag gct gag cag			1920
Gly Thr Val Pro Val Gln Leu Glu Gly Arg Ile Glu Gln Ala Glu Gln			
	625	630	635
gcc ctt cag gac att ctg gga gaa gct cag att tca gaa ggg gca atg			1968
Ala Leu Gln Asp Ile Leu Gly Glu Ala Gln Ile Ser Glu Gly Ala Met			
	645	650	655
aga gcc gtt gct gtc cgg ctg gcc aag gca agg agc caa gag aac gac			2016
Arg Ala Val Ala Val Arg Leu Ala Lys Ala Arg Ser Gln Glu Asn Asp			
	660	665	670
tac aag acc cgc ctg gat gac ctc aag atg act gca gaa agg atc cgg			2064
Tyr Lys Thr Arg Leu Asp Asp Leu Lys Met Thr Ala Glu Arg Ile Arg			
	675	680	685

gcc	ctg	ggc	agt	cag	cat	cag	aac	aga	gtt	cag	gat	acg	agc	aga	ctc	2112
Ala	Leu	Gly	Ser	Gln	His	Gln	Asn	Arg	Val	Gln	Asp	Thr	Ser	Arg	Leu	
690						695					700					
atc	tct	cag	atg	cgc	ctg	agt	ctg	gca	gga	agc	gaa	gct	ctc	ttg	gaa	2160
Ile	Ser	Gln	Met	Arg	Leu	Ser	Leu	Ala	Gly	Ser	Glu	Ala	Leu	Leu	Glu	
705					710					715					720	
aac	act	aat	atc	cat	tct	tct	gag	cac	tac	gtg	ggg	ccg	aat	gat	ttt	2208
Asn	Thr	Asn	Ile	His	Ser	Ser	Glu	His	Tyr	Val	Gly	Pro	Asn	Asp	Phe	
				725					730					735		
aaa	agt	ctg	gct	cag	gag	gct	aca	aga	aag	gca	gac	agc	cac	gct	gag	2256
Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Lys	Ala	Asp	Ser	His	Ala	Glu	
			740					745						750		
tca	gct	aac	gca	atg	aag	caa	cta	gca	agg	gaa	act	gag	gac	tac	tcc	2304
Ser	Ala	Asn	Ala	Met	Lys	Gln	Leu	Ala	Arg	Glu	Thr	Glu	Asp	Tyr	Ser	
		755					760					765				
aaa	caa	gca	ctt	tca	ttg	gcc	cgc	aag	ctc	ttg	agt	gga	gga	ggc	gga	2352
Lys	Gln	Ala	Leu	Ser	Leu	Ala	Arg	Lys	Leu	Leu	Ser	Gly	Gly	Gly	Gly	
	770					775					780					
agt	ggc	tct	tgg	gac	agc	tcc	gtg	gta	caa	ggg	ctt	atg	gga	aaa	tta	2400
Ser	Gly	Ser	Trp	Asp	Ser	Ser	Val	Val	Gln	Gly	Leu	Met	Gly	Lys	Leu	
785					790					795					800	
gag	aaa	acc	aag	tcc	ctg	agc	cag	cag	ctg	tca	ttg	gag	ggc	acc	caa	2448
Glu	Lys	Thr	Lys	Ser	Leu	Ser	Gln	Gln	Leu	Ser	Leu	Glu	Gly	Thr	Gln	
				805					810					815		
gcc	gac	att	gaa	gct	gat	agg	tcg	tat	cag	cac	agt	ctc	cgc	ctc	ctg	2496
Ala	Asp	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser	Leu	Arg	Leu	Leu	
			820					825					830			
gat	tct	gcc	tct	cag	ctt	cag	gga	gtc	agt	gat	ctg	tcc	ttt	cag	gtg	2544
Asp	Ser	Ala	Ser	Gln	Leu	Gln	Gly	Val	Ser	Asp	Leu	Ser	Phe	Gln	Val	
		835					840					845				
gaa	gca	aag	agg	atc	aga	caa	aag	gct	gat	tct	ctc	tca	aac	ctg	gtg	2592
Glu	Ala	Lys	Arg	Ile	Arg	Gln	Lys	Ala	Asp	Ser	Leu	Ser	Asn	Leu	Val	
	850					855					860					
acc	aga	caa	acg	gat	gca	ttc	acg	cgt	gtg	cga	aac	aat	ctg	ggg	aac	2640
Thr	Arg	Gln	Thr	Asp	Ala	Phe	Thr	Arg	Val	Arg	Asn	Asn	Leu	Gly	Asn	
865					870					875				880		
tgg	gaa	aaa	gaa	aca	cgg	cag	ctt	tta	cag	act	gga	aag	gat	agg	aga	2688
Trp	Glu	Lys	Glu	Thr	Arg	Gln	Leu	Leu	Gln	Thr	Gly	Lys	Asp	Arg	Arg	
				885					890					895		
cag	act	tca	gat	cag	ctg	ctt	tcc	cgt	gcc	aac	ctt	gct	aaa	aac	aga	2736
Gln	Thr	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn	Leu	Ala	Lys	Asn	Arg	
			900					905					910			
gcc	caa	gaa	gcg	cta	agt	atg	ggc	aat	gcc	act	ttt	tat	gaa	gtt	gag	2784
Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr	Phe	Tyr	Glu	Val	Glu	
	915						920					925				

aac atc ctg aag aac ctc cga gag ttt gat ctg cag gtt gaa gac aga Asn Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu Gln Val Glu Asp Arg 930 935 940	2832
aaa gca gag gct gaa gag gcc atg aag aga ctc tcc tct att agc cag Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu Ser Ser Ile Ser Gln 945 950 955 960	2880
aag gtt gcg gat gcc agt gac aag acc cag caa gca gaa acg gcc ctg Lys Val Ala Asp Ala Ser Asp Lys Thr Gln Gln Ala Glu Thr Ala Leu 965 970 975	2928
ggg agc gcc act gcc gac acc caa cgg gca aag aac gca gct agg gag Gly Ser Ala Thr Ala Asp Thr Gln Arg Ala Lys Asn Ala Ala Arg Glu 980 985 990	2976
gcc ctg gag atc agc agc gag ata gag ctg gag ata ggg agt ctg aac Ala Leu Glu Ile Ser Ser Glu Ile Glu Leu Glu Ile Gly Ser Leu Asn 995 1000 1005	3024
ttg gaa gct aat gtg aca gca gat ggg gcc ttg gcc atg gag aaa ggg Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu Ala Met Glu Lys Gly 1010 1015 1020	3072
act gcc act ctg aag agc gag atg aga gag atg att gag ctg gcc aga Thr Ala Thr Leu Lys Ser Glu Met Arg Glu Met Ile Glu Leu Ala Arg 1025 1030 1035 1040	3120
aag gag ctg gag ttt gac acg gat aag gac acg gtg cag ctg gtg att Lys Glu Leu Glu Phe Asp Thr Asp Lys Asp Thr Val Gln Leu Val Ile 1045 1050 1055	3168
act gaa gcc cag caa gct gat gcc aga gcc acg agt gcc gga gtt acc Thr Glu Ala Gln Gln Ala Asp Ala Arg Ala Thr Ser Ala Gly Val Thr 1060 1065 1070	3216
atc caa gac acr ctc aac aca ttg gac ggc atc cta cac ctc ata gac Ile Gln Asp Xaa Leu Asn Thr Leu Asp Gly Ile Leu His Leu Ile Asp 1075 1080 1085	3264
cag cct ggc agt gtg gat gaa gaa ggg atg atg cta tta gaa caa ggg Gln Pro Gly Ser Val Asp Glu Glu Gly Met Met Leu Leu Glu Gln Gly 1090 1095 1100	3312
ctt ttc caa gcc aag acc cag atc aac agt cga ctt cgg ccc ttg atg Leu Phe Gln Ala Lys Thr Gln Ile Asn Ser Arg Leu Arg Pro Leu Met 1105 1110 1115 1120	3360
tct gac ctg gag gag agg gtg cgt cgg cag agg aac cac ctc cat ctg Ser Asp Leu Glu Glu Arg Val Arg Arg Gln Arg Asn His Leu His Leu 1125 1130 1135	3408
ctg gag act agc ata gat gga att ctt gct gat gtg aag aac ctg gag Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu Glu 1140 1145 1150	3456
aac att cga gac aac ctg ccc cca ggc tgc tac aat acc caa gct ctt Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln Ala Leu 1155 1160 1165	3504
gag caa cag tgaagttgtc atagagattt gtccactgtt gtgaaaggac	3553

Glu Gln Gln
1170

acagacctca ggggtcagga gccatctcgt gtggatgggc tgtgctcagg ctatctgaac 3613
acatttaatg ggtttgttca ggtccaattc catccctgag accatgggct gtggatgtct 3673
tcctgtacca atataatact gtttgtaact cctgatgctg gcagtgaggc agatagcatt 3733
gagtatgaga ttgatcaagg agggacaaat cgtgcgctca gaacagtgaac aaactgaatt 3793
ctgggcagtg aggcagatag cattgagtat gagattgatc aaggacctgg accccaaaga 3853
tagactggat ggaaagacaa actgcacagg cagatgtttg cctcataata gtcgtaagtg 3913
gagtcctgga atttggtcag aacagtgaac aactggaatt ctgggatata gaaagatcct 3973
gctgctatgt caggacaaag tgagatctaa tcccgtcgc gccagcaaag tactcttgct 4033
tcacccacta gacgtttttt gtccaccaca tttcctccag tgcccacca atacatgagt 4093
atgtcctcca cttcatgctg agtgcagaga gcagtgatgg tatagatctg gaaatctggc 4153
ccatgtggag cagtgggtgcc cgctgcacc cctaaccctc atgctctcgg cctgagtgtg 4213
acagcctttc tcctaattgt gcgaacaact tagaggctgt atttttttat gaaagcatct 4273
tttaccagcc aagcaatcat tgggaaagta tttctttgag tttcaaagtg atataagaaa 4333
tgtgtctggc actaaaggaa gtggagttat ctaaaagata tattcatcat aatccaatct 4393
tccttttgaa aactaaaac tcatatacat ctgtgtattg tatcttattt tctctttctc 4453
ctctctcttt cctccacca taataagaga atgttcctac tcacacttca gctgggtcac 4513
atccatccct ccattcatcc ttccatccat ctttccatcc attacctcca tccagccttc 4573
taacatatat ttattgcgtc actactgtgt gccaggggtg agtgggaacag tatggacagt 4633
ctctactctc atggagttga gtgtctagtg agagaacaac attagaataa gtaaattggaa 4693
actcccatgc cttgttcatc tcatgtgata tttattgcag tcacccacc tttggtttga 4753
aacctctttt cttaataatg tgttgcaaga cattcccatg agggacttg agttagagca 4813
aagttgagat cgctctgagt tgtacacatt tctctatgtt ccagccgtct ctccaccct 4873
tccacacaga ctgtgcacag actggtgcat cagggcaata ccagtgggaa ttgctgaagg 4933
aaccagaggc attgggacct cagtttgga gactactgta ctgtctcacc tctgtacttc 4993
cttgtctttt catggatgtg ttattaaata aagaacgagt gttagatgct aaaaaaaaaa 5053
aaaa 5057

<210> 36
<211> 1171
<212> PRT
<213> Mus musculus

<400> 36

Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys
1 5 10 15
Val Phe Asp Gln Glu Leu His Arg Gln Ala Gly Ser Gly Phe Arg Cys
20 25 30
Leu Asn Cys Asn Asp Asn Thr Ala Gly Val His Cys Glu Arg Ser Arg
35 40 45
Glu Gly Phe Tyr Gln His Gln Ser Lys Ser Arg Cys Leu Pro Cys Asn
50 55 60
Cys His Ser Lys Gly Ser Leu Ser Ala Gly Cys Asp Asn Ser Gly Gln
65 70 75 80
Cys Arg Cys Lys Pro Gly Val Thr Gly Gln Arg Cys Asp Gln Cys Gln
85 90 95
Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys Thr Arg Asp Gln Gly
100 105 110
Gln Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala Gly Ile Ser Gly Pro
115 120 125
Cys Asp Ser Gly Arg Cys Val Cys Lys Pro Ala Val Thr Gly Glu Arg
130 135 140
Cys Asp Arg Cys Arg Pro Arg Asp Tyr His Leu Asp Arg Ala Asn Pro
145 150 155 160
Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His Ser Ala Ser Cys His
165 170 175
Ala Ser Ala Asp Phe Ser Val His Lys Ile Thr Ser Thr Phe Ser Gln
180 185 190
Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn Gly Ala Pro Ala Lys
195 200 205
Leu His Trp Ser Gln Arg His Arg Asp Val Phe Ser Ser Ala Arg Arg
210 215 220
Ser Asp Pro Val Tyr Phe Val Ala Pro Ala Lys Phe Leu Gly Asn Gln
225 230 235 240
Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp Tyr Arg Val Asp Arg
245 250 255
Gly Gly Arg Gln Pro Ser Ala Tyr Asp Val Ile Leu Glu Gly Ala Gly
260 265 270
Leu Gln Ile Arg Ala Pro Leu Met Ala Pro Gly Lys Thr Leu Pro Cys
275 280 285
Gly Ile Thr Lys Thr Tyr Thr Phe Arg Leu Asn Glu His Pro Ser Ser
290 295 300
His Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr Arg Arg Leu Leu Arg
305 310 315 320

Asn Leu Thr Ala Leu Leu Met Ile Arg Ala Thr Tyr Gly Glu Tyr Ser
325 330 335

Thr Gly Tyr Ile Asp Asn Val Thr Leu Val Ser Ala Arg Pro Val Leu
340 345 350

Gly Ala Pro Ala Pro Trp Val Glu Arg Cys Val Cys Leu Leu Gly Tyr
355 360 365

Lys Gly Gln Phe Cys Gln Glu Cys Ala Ser Gly Tyr Lys Arg Asp Ser
370 375 380

Ala Arg Leu Gly Ala Phe Gly Ala Cys Val Pro Cys Asn Cys Gln Gly
385 390 395 400

Glu Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu
405 410 415

Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp
420 425 430

Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe
435 440 445

Ser Cys Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys
450 455 460

Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Phe
465 470 475 480

Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Arg
485 490 495

Cys Gln Cys Asn Asn Asn Val Asp Pro Asn Ala Ser Gly Asn Cys Asp
500 505 510

Gln Leu Thr Gly Arg Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Val
515 520 525

Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro
530 535 540

Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Ser Pro Met Gly Ala
545 550 555 560

Glu Pro Gly Glu Cys Arg Gly Asp Gly Ser Cys Val Cys Lys Pro Gly
565 570 575

Phe Gly Ala Phe Asn Cys Asp His Ala Ala Leu Thr Ser Cys Pro Ala
580 585 590

Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Thr Gln Gln Leu
595 600 605

Gln Ser Leu Glu Ala Leu Val Ser Lys Ala Gln Gly Gly Gly Gly Gly
610 615 620

Gly Thr Val Pro Val Gln Leu Glu Gly Arg Ile Glu Gln Ala Glu Gln
625 630 635 640

Ala Leu Gln Asp Ile Leu Gly Glu Ala Gln Ile Ser Glu Gly Ala Met

645					650					655						
Arg	Ala	Val	Ala	Val	Arg	Leu	Ala	Lys	Ala	Arg	Ser	Gln	Glu	Asn	Asp	
660					665					670						
Tyr	Lys	Thr	Arg	Leu	Asp	Asp	Leu	Lys	Met	Thr	Ala	Glu	Arg	Ile	Arg	
675					680					685						
Ala	Leu	Gly	Ser	Gln	His	Gln	Asn	Arg	Val	Gln	Asp	Thr	Ser	Arg	Leu	
690					695					700						
Ile	Ser	Gln	Met	Arg	Leu	Ser	Leu	Ala	Gly	Ser	Glu	Ala	Leu	Leu	Glu	
705					710					715					720	
Asn	Thr	Asn	Ile	His	Ser	Ser	Glu	His	Tyr	Val	Gly	Pro	Asn	Asp	Phe	
725					730					735						
Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Lys	Ala	Asp	Ser	His	Ala	Glu	
740					745					750						
Ser	Ala	Asn	Ala	Met	Lys	Gln	Leu	Ala	Arg	Glu	Thr	Glu	Asp	Tyr	Ser	
755					760					765						
Lys	Gln	Ala	Leu	Ser	Leu	Ala	Arg	Lys	Leu	Leu	Ser	Gly	Gly	Gly	Gly	
770					775					780						
Ser	Gly	Ser	Trp	Asp	Ser	Ser	Val	Val	Gln	Gly	Leu	Met	Gly	Lys	Leu	
785					790					795					800	
Glu	Lys	Thr	Lys	Ser	Leu	Ser	Gln	Gln	Leu	Ser	Leu	Glu	Gly	Thr	Gln	
805					810					815						
Ala	Asp	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser	Leu	Arg	Leu	Leu	
820					825					830						
Asp	Ser	Ala	Ser	Gln	Leu	Gln	Gly	Val	Ser	Asp	Leu	Ser	Phe	Gln	Val	
835					840					845						
Glu	Ala	Lys	Arg	Ile	Arg	Gln	Lys	Ala	Asp	Ser	Leu	Ser	Asn	Leu	Val	
850					855					860						
Thr	Arg	Gln	Thr	Asp	Ala	Phe	Thr	Arg	Val	Arg	Asn	Asn	Leu	Gly	Asn	
865					870					875					880	
Trp	Glu	Lys	Glu	Thr	Arg	Gln	Leu	Leu	Gln	Thr	Gly	Lys	Asp	Arg	Arg	
885					890					895						
Gln	Thr	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn	Leu	Ala	Lys	Asn	Arg	
900					905					910						
Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr	Phe	Tyr	Glu	Val	Glu	
915					920					925						
Asn	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu	Gln	Val	Glu	Asp	Arg	
930					935					940						
Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu	Ser	Ser	Ile	Ser	Gln	
945					950					955					960	
Lys	Val	Ala	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln	Ala	Glu	Thr	Ala	Leu	
965					970					975						

Gly Ser Ala Thr Ala Asp Thr Gln Arg Ala Lys Asn Ala Ala Arg Glu
980 985 990

Ala Leu Glu Ile Ser Ser Glu Ile Glu Leu Glu Ile Gly Ser Leu Asn
995 1000 1005

Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu Ala Met Glu Lys Gly
1010 1015 1020

Thr Ala Thr Leu Lys Ser Glu Met Arg Glu Met Ile Glu Leu Ala Arg
1025 1030 1035 1040

Lys Glu Leu Glu Phe Asp Thr Asp Lys Asp Thr Val Gln Leu Val Ile
1045 1050 1055

Thr Glu Ala Gln Gln Ala Asp Ala Arg Ala Thr Ser Ala Gly Val Thr
1060 1065 1070

Ile Gln Asp Xaa Leu Asn Thr Leu Asp Gly Ile Leu His Leu Ile Asp
1075 1080 1085

Gln Pro Gly Ser Val Asp Glu Glu Gly Met Met Leu Leu Glu Gln Gly
1090 1095 1100

Leu Phe Gln Ala Lys Thr Gln Ile Asn Ser Arg Leu Arg Pro Leu Met
1105 1110 1115 1120

Ser Asp Leu Glu Glu Arg Val Arg Arg Gln Arg Asn His Leu His Leu
1125 1130 1135

Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu Glu
1140 1145 1150

Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln Ala Leu
1155 1160 1165

Glu Gln Gln
1170